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Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                   SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vrdent:*
12: sp_vrus:*
13: sp_vrtebrate:*
14: sp_urlassified:*
15: sp_archeap:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
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1547
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                                                                                                                 sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
SUMMARIES
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Result No.	Score	Query Match	query Query Match Length	DB	Ħ	Description
1	1515	97.9	298	۱ ه	Q8SQH5	Q8sqh5 bos taurus
jų	1450	93.7	298	1	OIHUBO	Q8jhj0 brachydanio
ω	1446	93.5	298	<u>۔</u>	Q9PRH1	Oprhi rana rugosa
4	1443	93.3	298	13	Q9PRH2	
₅	1443	93.3	298	13	Q8AYM3	3 gall
0	1439	93.0	298	13	Q9YIC4	H2
7	1425	92.1	298	13	Q919M9	Q9i9m9 xenopus lae
8	1423	92.0	298	σ	046373	O46373 oryctolagus
9	1417	91.6	298	11	Q8BVI9	Q8bvi9 mus musculu
10	1295	83.7	317	13	Q91336	Q91336 rana sylvat
11	1278	82.6	299	v	Q95VX4	Q95vx4 ethmostigmu
12	1253.5	81.0	312	თ	Q8IRA0	Q8ira0 drosophila
13	1248.5	80.7	300	v	Q9NHW5	Q9nhw5 lucilia cup
14	1190.5	77.0	288	υı	044093	O44093 drosophila
15	1185.5	76.6	288	σ	044094	O44094 drosophila
16	1146	74.1	254	11	Q8BKQ5	Q8bkq5 mus musculu

4 4 5	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
749.5	750	752	753	755	759	764.5	778	819	915	919	925	929	932	938	939	942	949.5	950.5	983	985	986	1029	1029	1032	1040.5	1102	1125.5	1145.5
48.4	48.5	48.6	48.7	48.8	49.1	49.4	50.3	52.9	59.1	59.4	59.8	60.1	60.2	60.6	60.7	60.9	61.4	61.4	63.5	63.7	63.7	66.5	66.5	66.7	67.3	71.2	72.8	74.0
306	386	307	317	303	326	302	305	170	308	306	308	305	301	301	301	301	307	318	300	309	300	313	313	300	310	315	307	304
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Q18683	P93767	076286	Q9N647	074260	P91270 .	Q8J0M2	Q9P8M1	Q9XS69	Q8MVR6	Q8MVR5	QBMVRB	Q8MVR7	Q8MVR4	Q26006	Q25692	Q8IJ34	Q9XM22	Q9BJ36	Q17407	097470	001813	P91410	Q21103	045865	Q8H727	Q9H0C2	062526	Q25129
	7	. 076286 trypanosoma	Q9n647 leishmania	074260 candida par	P91270 caenorhabdi		Q9p8ml yarrowia li	Q9xs69 sus scrofa	Q8mvr6 nyctotherus	Q8mvr5 nyctotherus	Q8mvr8 nyctotherus	Q8mvr7 nyctotherus				Q8ij34 plasmodium				_	O01813 caenorhabdi	P91410 caenorhabdi	Q21103 caenorhabdi	O45865 caenorhabdi	Q8h727 phytophthor	Q9h0c2 homo sapien		Q25129 halocynthia

ALIGNMENTS

•	RESULT Q8SQH5	
	ij	Q8SQH5 PRELIMINARY; PRT; 298 AA.
	AC	
	ij	(TrEMBLrel.
	Δī	(TrEMBLrel. 21,
	ဌ	(TrEMBLrel. 23, Last annotation
	DE	leotide translocator 2
	တ္ထ	rus (Bovine)
	გ	ryota; N
	8	Cetartiodactyla; Run
	റ്റ	
	×	I_TaxI
	R	[1]
	RP	SEQUENCE FROM N.A.
	RA	Yamazaki N., Shinohara Y., Tanida K., Terada H.;
	RT	Ζ.
	R.T	identification of possible amino acids that determine functional
	RT	
	뫈	Mitochondrion 1:371-379(2002).
	DR	BMBL; AB065433; BAB84673.1;
	묫	InterPro; IPR001993; Mitoch_carrier.
	DR	Pfam; PF00153; mito_carr; 3.
	DR	PROSITE; PS00215; MITOCH CARRIER; 3.
	SO	SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;
	Sug.	y Match 97.9%; Score 151:
	Matc	Hebt Local Similarity 97.7%; Freq. No. 5.2e-126; Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
	Ş	1 MTDAALSAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
	망	1 MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
	Ş	61 IPKBQBVLSFWRGNLANVIRYFBTQALNBAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
	망	61 IPKEQGYLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
	Ş	121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180

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RESULT 3
Q9PRH1
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Best Local
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Nat. Genet. 31:135-140(2002).
EMBL; AF506216; AAM34660.1;
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00784; MTUNCOUPLING.
PROSITE; PS00784; MTOCH_CARRIER; 3.
SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Q8JHI0;
01-OCT-2002
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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G., Amsterdam A., Sun Z., Antonelli M.,
S., Haldi M., Artzt K., Farrington S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYEGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGITSYPFDTVRRRMM
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92.9%;
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Last sequence update)
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Pred. No. 3e-120;
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Q9PRH1

PRELIMINARY;

PRT;

298

B

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RESULT 4
Q9PRH2
ID Q9PR
AC Q9PR
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
CO Rana
OC Euka
OC Amph
OX NCBII
RN [1]
RN [1]
RN MEDL
RA MEDL
RA MIUX
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Best Local S
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A Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

A Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

I "The origin and differentiation of the heteromorphic sex

Z, W, X, and Y in the frog Rana rugosa, inferred from the

a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

L Mol. Biol. Evol. 15:1612-1619(1998).

I SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI

R EMBL; AB008463; BAA36513.1; -.

R EMBL; AB008461; BAA36511.1; -.

R EMBL; AB008462; BAA36511.1; -.

R EMBL; AB008462; BAA36512.1; -.

R EMBL; AB008462; BAA36511.1; -.

R EMBL; AB008461; BAA3651.1; -.
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                                                                                                                                                                                                                                                                                            Q9PRH2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
SEQUENCE FROM N.A.
MEDLINE=99083429; PubMed=9866197;
Miura I., Ohtani H., Nakamura M.,
                                                                                                                             Eukaryota; Metazoa; (Amphibia; Batrachia; NCBI_TaxID=8410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana rugosa (Wrinkled frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                    Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                     ADP/ATP translocase.
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Last ann
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Neobatrachia; Ranoidea;
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Last annotation updat
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Pred. No. 6.8e
14; Mismatches
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      Ichikawa
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Ranidae; Rana.
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Ranidae; Rana
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Matches 275
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Matches 272; Conser
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REMBL; AB008450; BAA36510.1; -.
REMBL; AB008458; BAA36509.1; -.
REMBL; AB008459; MATOCACARIER.
REMBL; AB008459; MITOCACRRIER.
REMBL; AB008459; MITOCACRRIER.
REMBL; AB008459; MITOCACRRIER.
REMBL; PR00725; MITOCACRRIER.
REMBL; AB008459; BAA36509.1; -.
REMBL; AB008459; B
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Q8AYM3;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                         FEBS Lett.
EMBL; AB08
                                                                                                                                                                                                                                                                                                                                                      AVANT.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                        Toyomizu M., Ueda M., Sato S., Seki Y., Sal
"Cold-induced mitochondrial uncoupling and
and ANT mRNA in chicken skeletal muscle.",
FEBS Lett. 0.0-0(2002).
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Mol. Biol. Ev
                                                                                                                                                                       SEQUENCE
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                                                                    Local 275;
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Biol. Evol. 15:1612-1619(1998).
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                                                                                                                                                                     AB088686; BAC15533.1; -.
NCE 298 AA; 32847 MW;
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                       MTDAALSFAKDFLAGGVAAAISKTAVAFIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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MADQAISFLKDFLARGVAAAISKTAVAPIBRVKLLLQVQHASKQIAADKQYKGIIDCVVR
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3 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                      Conservative
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                                                                                                     93.3%;
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                                                                                 Score 1443; DB 13;
Pred. No. 1.2e-119;
9; Mismatches 12;
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Pred. No. 1.2e
5; Mismatches
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1.2e-119;
ches 10;
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Matches 271
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
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Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic s
Z, W, X, and Y in the frog Rana rugosa, inferred from
a sex-linked gene, ADP/ATP translocase.";
Mol. Biol. Evol. 15:1612-1619(1998).
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Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33068 MW; 15827
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Rana rugosa (Wrinkled frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Q9YIC4;
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QSGRKGABIMYSGTIDCWKKIARDEGSRAFFKGAWSNVLRGMGGAFVLVLYDELKKY
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Last annotation update)
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Pred. No. 2.8e-119;
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"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
Tynamic Patterns of Expression During Development.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AF231347; AAP63471.1; -.

RR InterPro; IPR001993; Mitoch carrier.

InterPro; IPR001993; Mitoch carrier.

InterPro; IPR002067; Mit_carrier.

InterPro; IPR002067; Mit_carrier.

InterPro; IPR002030; Mit_uncoupling.

Pfam; PF00153; mitocarr; 3.

RR PF1NTS; PR00926; MITOCH CARRIER.

PRINTS; PR00926; MITOCH CARRIER.

PROSITE; PS007215; MITOCH CARRIER; 3.

Membrane; Transmembrane; Transport.

SEQUENCE 298 AA; 32940 MM; 91B740133751877F CRC64;
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Q919M9;
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01-JUN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                            ADP/ATP translocase.
Oryctolagus cuniculus (Rabbit)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Lagomorpha
        SEQUENCE FROM N.A.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
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                                                                                                                    Chordata; Craniata; Vei
Lagomorpha; Leporidae;
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91.6%;
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Pred. No. 4.9e
11; Mismatches
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Best Local Sin
Matches 266;
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Matches 2
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Q8BVI9;
01-MAR-2003 (TrEMBLrel. 23, C:
01-MAR-2003 (TrEMBLrel. 23, L:
01-MAR-2003 (TrEMBLrel. 23, L:
Solute carrier family 25.
                                                                                                                                  STRAIN-C57BL/6J; TISSUE-Medulla oblongata;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
the RIXEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annota
60,770 full-length cDNAs.";
Nature 420.563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaguchi N., Kasai M.;
"Identification of a 30kDa calsequestrin-binding protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skeletal muscle.";
J. Biochem. 335:541-547(1998)
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mús musculus (Mouse)
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                                                                                              298 AA;
Conservative
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                     91.6%;
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89.9%; Pred. No. 7.4e-118;
bive 16; Mismatches 14;
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Last annotation updat
  Score 1417; D
Pred. No. 2.5e
L5; Mismatches
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Sciurognathi; Muridae;
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                     7; DB 11;
2.5e-117;
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Q91336;
01-NOV-1996
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PROSITE; PS00215; MITOCH_CARRIER; 3.

Membrane; Transmembrane; Transport.

SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cai Q., Storey K.B.;
Submitted (APR-1999) to t
-i- SIMILARITY: BELONGS T
EMBL; U44832; AAA97882.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97398141; PubMed=9256066; Cai Q., Greenway S.C., Storey K.B.; "Differential regulation of the mitochondrial ADP/ATP in wood frogs under freezing stress."; Blochim. Blophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana sylvatica (Wood frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
NCBI_TaxID=45438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PP00153; mito_carr; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKAGAGREFNGLGDCLAKIFKSDGLKGLYQGFNVS
                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVK1YKSDG1KGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                               MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFVSWMIAQSVTAVAGFGSYPFDTVRRRMM
                                 VQGIIIYRAAYFGIYDTAXGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                                                                                                                                                                                                                   IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                              I PKEQGF I SFWRGNLANVIRYF PTQALNFGFKDKYKKI FLDNVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                 MTDAANSFAKDFLAGGVAAAISKTAVAPIERVKLLVQVQHASKQITADKQYKGIMDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAMSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRNMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I PKEQEVLS FWRGNLANV I RYFPTQALMFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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90.1%;
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Last
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Pred. No. 1.7e-106;
4; Mismatches 13;
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annotation update)
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CARRIER FAMILY.
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ID Q95VX
AC Q95VY
AC Q95VY
DT 01-DE
DT 01-M2
DT 01
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Q95VX4;
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RESULT 12
Q8IRAO
ID Q8IRA
AC Q8IRA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
CG169
GN SESB-.
OS Droso
OC Eukar
OC Eukar
OC Neopat
OC Neopat
OC Neopat
OC NCBI
RN (1]
RN (1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ethmostigmus rubripes.
Eukaryota; Metazoa; Art
Pleurostigmophora; Scol
NCBI_TaxID=62613;
                                                                                                                            Q8IRAO;
Q8IRAO;
01-MAR-2003
01-MAR-2003
01-MAR-2003
CG16944-PC:
                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL; AF401758; AAL02100.1;
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                                                                                                                                                                                                                                                                                                                KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
                                                                                                                                                                                                                                                                                                                                                                                   IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMNQSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKE
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                                                                                                                                                                                                                                                                                                 KKADÍLYKNTIDCWGKÍYKTEGGAAFFKGAFSNILRGTGGAFVLVLYDEIK
                                                                                                                                                                                                                                                                                                                                                              IIYRAAYFGTYDTAKGMLEDFKNTPIVISWLIAQTVTTCAGIISYFFDTVRRRMMQSGR
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                                                                                                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                PRELIMINARY;
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Last sequence update)
Last annotation updat
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Pred. No. 5.2e
22; Mismatches
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hockins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hockins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hockins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barlandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfelffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Marik H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Grerry J.M., Cawley S., Dahlke C., Davensort L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Nixon K. J., Li Z., Liang Y., Lin X.,
RA Harris N., Malley H., Marris N., Malley J., Li Z., Liang Y., Lin X.,
RA Melmon D.R., Nelson K.A., Nixon K., Musskern D.R., Mecheck
                                                                                                                                                                                                                                                                                                                                                                                                                                A Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.A.
Beanzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Conzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Welhon K.A., Nunco J.
A Pacleb J., Paragas V., Park S., Patel S., Ptelfer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
"Sequencing of Drosophila melanogaster genome.",

"Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A
                                              SEQUENCE FROM N.A.
Adams M.D., Celniker
Submitted (MAR-2000)
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                                                 Gibbs R.A., Rubin G.M., Venter C.J.; e EMBL/GenBank/DDBJ databases.
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S.M.,
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Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Lucilla cuprina (Brechbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
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01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Pred. No. 2.1e-102;
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RESULT 15
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EMBL; AF025798; AAB87883.1; -.

FlyBase; FB9n002302; Dpse\sesB.

InterPro; IPR00193; Mitoch_carrier.

InterPro; IPR00193; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.

PF00153; mito_carri_3.

PRLNTS; PR00926; MITOCH_CARRIER.

PROSITE; PS00926; MITOCH_CARRIER; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.

PROSITE; RS00eat; Transmembrane; Transport.

Membrane; Repeat; Transmembrane; Transport.

Membrane; Repeat; Transmembrane; Transport.

Membrane; Repeat; Transmembrane; Transport.

MON TER 288
288
SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Genetica 0:0-0(1997)
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Search completed: December Job time: 31.701 secs

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Matches 228;
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Membrane; Repeat; Transmembrane; Transport.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo'
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR002067; Mit_carrier.
Pfam; Pf00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF025799; AAB87884.1; -. FlyBase; FBgm0023237; Dsub\sesB.
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                                                                                                                       IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQSGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                    QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
KATEIIYKNTIHCWGTIAKQE-GTAFFKGAFSNVLRGTGGAFVLV
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P48962 mus musculu
P02722 bos taurus
P12235 homo sapien
Q26365 drosophila
Q27238 anopheles g
P31692 chlorella k
     P2703
P2703
Q09188
O22342
P102723
P1823
P40941
P047041
P047041
P047081
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P32007 bos taurus
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Q9qxx4 mus musculu				Q9ujs0 homo sapien							

ALIGNMENTS

3
Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Cararrhini; Hominidae; Homo.
Etimacas; cacatinini; nominicas;
SEQUENCE FROM N.A. MEDLINE=89236396; PubMed=2541251;
vick M.J., Walker J.E.;
P/ATP translocase.";
J. Mol. Biol. 206:261-280(1989). [2]
Margolin J.F.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
Eye, and Lung; ed=12477932;
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
B., Buetow K.H., Schaefer C.F., Bhat N.K.
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
nstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange (
McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
on E., Ketteman M., Madan A., Rodrigues S., lan A., Young A.C., Shevchenko Y., Bouffard
W., Touchman J.W., Green B.D., Dickson M.C., C., Grimwood J., Schmutz J., Myers R.M.
M.I., Ska
"Generation and initial analysis of more than 15,000 full-length
and mouse cDNA sequences.";
CI. ACAG. SCI. (
TISSUE-Liver;
24845; PubMed=2
"Two distinct genes for ADP/ATP translocase are expressed at the mRNA

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EMBL; AY007135; AAA36750.1,
EMBL; AY007135; AAG01998.1; -.
EMBL; BC007295; AAH07295.1; -.
EMBL; BC007850; AAH07850.1; -.
REMBL; BC008737; AAH08935.1; -.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 298; Conserv
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GO; 600:005744; C:mitochondrial inner membrane translocase
GO; GO:0005471; R:ATP/ADP antiporter activity; NAS.
GO; GO:000654; P:ATP/ADP exchange; TAS.
InterPro; IPR0020067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR002030; Mit_och carrier.
InterPro; IPR001993; Mitoch carrier.
Pfam; PP00153; mito carr; 3.
PRINTS; PR00784; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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EMBL; BC014775; AAH14775.1;
PIR; S03894; S03894
Genew; HCNC:10992; SLC25A6.
MIM; 300151;
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between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A.
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SUBUNIT: Homodimer.
SUBCELLITAR
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                          VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRWM
                                                                                                                                                         I PKEQGVLS FWRGNLANVI RYF PTQALNFA FKDKYKQI FLGGVDKHTQFWRYF AGNLASG
                                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                  I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                    MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner membrane;
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                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                        Score 1543;
Pred. No. 3.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                            KHTQ -> RHA (IN REF. 4)
S -> F (IN REF. 3; AAH1
; 18534E9F0E49672F CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
(POTENTIAL)
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(POTENTIAL).
(POTENTIAL).
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                              Query Match
Best Local Sim
Matches 291;
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                                                                                  REPEAT
REPEAT
SEQUENCE
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                                                                                                                                                                                                                                              PRINTS; PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
Biochemistry 28:866-873 (1999).
-!- FUNCTION: CATALIZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-!- SUBUNIT: Homodimer.
-!- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P32007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Boyine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyidae; Boyinae; Bos.
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Mitochondrion; Inner membrane; Repeat;
                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_
                                                                                                                                                                                                                                                                                               InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
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); PR00926; MITOCARRIER.
); PR00784; MITOCH CARRIER.
TE; PS00215; MITOCH CARRIER
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                                             Similarity
MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                     family.
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. 26, Last sequence update)
l. 40, Last annotation update
protein, isoform T2 (ADP/ATP
slocator 3) (ANT 3).
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                                            98.0%;
97.7%;
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                               Score 1512; DB 1;
Pred. No. 1.9e-125;
4; Mismatches 3;
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                                                                                   1C34E7DF6EDE4061 CRC64;
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(ADP/ATP
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                                                                                                                                                                                                                                   Transmembrane; Transport;
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MBL outstation -
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RESULT 3
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P05141; O43350;
13-AUG-1987 (Rel. 05, C
01-OCT-1994 (Rel. 30, I
28-FEB-2003 (Rel. 41, I
                                                                                  Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are
level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
MITOCHONDRIAL INNER MEMBRANE.
-1- SUBCHLIULAR LOCATION: Integral membrane prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87166056; PubMed=3031073;
MEDLINE=87166056; PubMed=3031073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,

Mazzarella R.A., Schlessinger D., Chen E.Y.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                          MEDLINE=88124845;
                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 47-298 FROM N.A. TISSUB=Liver;
                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Becker M., Graves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning of a cDNA for a human growth-regulated.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90375457; PubMed=2168878;
Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga I
"The human fibroblast adenine nucleotide translocator
cloning and sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLC25A5 OR ANT2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP
(Adenine nuclectide translocator 2) (ANT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
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          inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier
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GO; GO:005887; C:integral to plasma membrane; TAS.
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GO; GO:0015207; F:small molecule transport; TAS.
InterPro; IPR002057; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
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EMBL; AC004000; AAB96347.1; --
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PROSITE; PS00215; MITOCH CARRIER;
Mitochondrion; Inner membrane; Rep
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                                                                                         QSGRKGADIMYTGTVDCWRKI FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                      VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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MEDLINE-94002161; PubMed-8399300;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

"Isolation and characterization of cDNA clones and a genomic cencoding rat mitochondrial adenine nucleotide translocator.";

Biochim. Biophys. Acta 1152:192-196(193).

-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLC25A5 OR ANT2.
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st annotation update)
fibroblast isoform (ADP/ATP translocase
slocator 2) (ANT 2).
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Pred. No. 4
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Laplace C.;
Submitted (I
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p51881; 061311;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
ADP,ATP carrier protein, fibroblast isoform (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE=97059403; PubMed=8903724;
Ellison J.W., Li X., Francke U., Shapiro I
"Rapid evolution of human pseudoautosomal
                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                  This
                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. PubMed=10974536; MEDLINE=20432087; PubMed=10974536; Levy S.E., Chen Y.-S., Graham B.H. "Expression and sequence analysis translocase 1 and 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                     EMBL; U27316; AAC52838.1; -.
EMBL; U10404; AAA19099.1; -.
EMBL; X70847; CAA55196.1; -.
EMBL; AF240003; AAF64471.1; -.
                                                                            or send an
                                                                               entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                         Costet P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   hesis (1995), University
                                                                                                                                                                                                                           e 254:57-66(2000).
FUNCTION: CATALYZES
MITOCHONDRIAL INNER
                                                                                                                                                                      DOMAIN: COMPOSED OF SIMILARITY: Belongs
                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                               inner membrane
                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation
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f the mouse
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; Murinae; Mus
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5 outstation -
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MGI:1353496;

IPR002067;

Mit_carrier.

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RESULT 6
ADT1 RAT1
AC Q059
DT 01-F
DT 16-C
DE ADP,
DE TART
GN SLCZ
OS RATT
OC ENAR
OC MAMM
OC STRU
RR STRU
RC -1-
CC -1-
CC -1-
CC -1-
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Best Local
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Q05962;
01-FEB-1994
01-FEB-1994
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TRANSMEM
TRANSMEM
                                                                                                         STRAIN-Sprague-Dawley, and Wistar; TIS
MEDLINE-94002161; PubMed-8399300;
Shinohara Y., Kamida M., Yamazaki N.,
"Isolation and characterization of cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
                                                           encoding rat mitochondrial adenine nucleotide translocator.", Biochim. Biophys. Acta 1152:192-196(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
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PRINTS; PR00926; MITOCARRIER,
PRINTS; PR00784; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                    SLC25A4 OR ANT1
                                                                                                                                                                                                                                             01-PEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1
translocase 1) (Adenine nucleotide translocator 1) (ANT 1)
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Multigene fami
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inner membrane.
TISSUE SPECIFICITY: IN HEART,
EXTENT, IN BRAIN AND KIDNEY.
                                      SUBCELLULAR LOCATION: Integral
                                                    SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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209
298
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73
117
176
274
273
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                                                                                                                                                                                                                                                                                                                       STANDARD;
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231
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91.6%;
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                                                                                                                                               and Wistar; TISSUE=Heart,
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5; Mismatches
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Pred. No. 1.
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Sciurognathi; Muridae;
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(POTENTIAL).
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               SKELETAL
                                      membrane protein. Mitochondrial
                                                                                                              CDNA
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                                                                                                                          Terada H.;
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                                                                                                            genomic
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               A LESSER
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RESULT 7
ADT1 MUSE
ID ADT1 M
AC P48962
DT 01-FEB
DT 15-SEP
DE ADP, AT
DE trans1
GN SLC35A
OS Mus mu
OC Eukary
OC Mammall
OX NCBI_I
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                                                 ADT1 MOUSE STANDARD; PRT; 298 AA. P48962; Q62164; 01-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) ADP,ATP carrier protein, heart/skeletal muscle translocase 1) (Adenine nucleotide translocator SLC25A4 OR ANT1 OR ANC1.
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             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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EMBL; D12770; BAA02237.1;
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InterPro; IPR002030; Mit_uncoupling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I60173; I60173
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267; Conserv
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                                                                                                                                                                                                              QSGRKGADIMYTGTVDCWRKIAKDEGRKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
                                                                                                                                                                                                                              QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAKGMLFDPKNTHIVVSWMIAQTVTAVAGVVSYFFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTK1FKSDGLKGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                          MGDQALSFLKDFLAGGIAAAVSKTAVAPIBRVKLLLQVQHASKQISABKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
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             Chordata;
Rodentia;
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brane; Repeat;
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Pred. No. 16
             Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                           Euteleostomi;
             Murinae;
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                                                                 (ADP/ATP) (mANC1).
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Mozley K.Ctteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schwintz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schwintz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schwintz J., Myers R.M.,
RA Rodriguez A.C., Srevylinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

Generation A. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                               EMBL; U27315; AAC52837.1; -.
EMBL; X74510; CAA52616.1; -.
EMBL; AP2440002; AAF64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC026925; AAH26925.1; -.
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as 100 may modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=97059403; PubMed=8903724;
Ellison J.W., Li X., Francke U., Shapiro L.J.;
"Rapid evolution of human pseudoautosomal genes and their mouse
                      InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;

"Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laplace C., Costet P.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                           PIR; S37210; S37210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                      MGI:1353495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane.
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    PS00215;
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MITOCH_CARRIER;
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RESULT
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Multigene family
TRANSMEM 12
TRANSMEM 73
TRANSMEM 117
TRANSMEM 117
TRANSMEM 176
TRANSMEM 214
TRANSMEM 273
                                                                                                                                                                                                                                                                                                                                       ADT1 BOVIN
P02722;
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CONFLICT
SEQUENCE
                                                                                                                               MEDLINE-8922903; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial ADI differences in various tissues."; Bischemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase
(Adenine nucleotide translocator 1) (ANT 1).
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REPEAT
                                                                SEQUENCE.

MEDILINE=82188267; PubMed=7076130;

Aquila H., Misra D., Eulitz M., Klingenberg Normplete amino acid sequence of the ADP/ATP mitochondria.";
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                BOVIN
          SEQUENCE OF 207-2: MEDLINE=86295775; Rasmussen U.B., W.
                                            Hoppe-Seyler'в
[3]
                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89229093;
                                                                                                                                                                                                                                                                     SLC25A4 OR ANT1.
                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                            Bos taurus (Bovine).
"Bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                  OF 207-297
                                                                                                                                                                                                                                                                                                                                                                                                                          QSGRKGADIMYTGTVDCWRKIFRDEGGKAPFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                      z. Physiol.
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                                                                                                                                                                                                                                                                                                                                                     STANDARD;
            Wohlrab H.
                      PubMed=3017341;
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                                                      Chem. 363:345-349(1982)
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Pred. No. 3.
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3A849FEAB0981462
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                                                                                                                                                                                                                                                                                                                                                     297
                                                                                                                                                                     Walker J.E.;
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RESULT 9
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ID ADT1_HUMAN
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INIT_MET
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MOD_RES
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PRINTS; PR00784; MITUNCOUPLING.
PR00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 138:850-857(1-1-FUNCTION: CATALYZES THE EXCHANGE OF ADP
MITOCHONDRIAL INNER MEMBRANE.
-1- SUBUNIT: Homodimer.
-1- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupil
InterPro; IPR001993; Mitoch_carri
Pfam; PP00153; mito_carr; 3
PRINTS; PR00926; MITOCARRIER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the mitochondrial carrier family.
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                                                                                                                                                                                                                                                       QGIIIYRAAYFGVYDTAKGMLFDFKNTHIVVSWMIAQTVTAVAGVVSYFFDTVRRRMMMQ 241
                                                                                                                                                                                                                                                                                                                                   AAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRI
                                                                                                                                                               SGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAMSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                         QGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGL
                                                                                                                                                                                                                                                                                                                                                                                                                        PKEQGVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGG
                                                                                                                                                                                                                                                                                                            AAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSV
                                                                                                                                                                                                                                                                                                                                                                                                    PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDOALSFLKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRI
                                                                                                                                   SGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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72
116
175
175
213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane; Repeat; Transmembrane; Transport;
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3'-noncoding sequence.";
Res. Commun. 138:850-857(1986)
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.90
133
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89.2%;
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Pred. No. 4.1e
19; Mismatches
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1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
1.
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2.
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                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1417; DB 1;
No. 4.1e-117;
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WBL outstation -
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RA Strausberg R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Romstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., RA Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., RA Richards J., Worley A.C., Shevchenko Y., Bouffard G.G., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Hakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", L. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE rkum w.r..
MEDLINE-88041149; PubMed=2823266;
MEDLINE-88041149; PubMed=2823266;
Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
"CDNA sequence of a human skeletal muscle ADP/ATP translocator:
of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator of a leader peptide from a leader peptide fr
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MEDLINE=89340499; PubMed=2547778;

Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;

Fukuyama R., Maekawa M., Shimizu Y., Shimizu Y.,

Thuman muscle adenine nucleotide translocator gene has four of the state 
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MEDLINE-89236396; PubMed=2541251;
MEDLINE-89236396; PubMed=2541251;
MEDLINE-89236396; PubMed=2541251;
MEDLINE-89236396; PubMed=2541251;
MEDLINE-89236396; PubMed=2541251;
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01-NCY-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle
translocase 1) (Adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequences of two expressed ADP/ATP translocase.";
                                                                                                        Kaukonen J., Juselius J.K., Tiranti
Comi G.P., Keranen J., Peltonen L.,
                                                                                                                                                                                    MEDLINE=20385067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates;
                                    "Role of adenine nucleotide translocator Science 289:782-785(2000).
                                                                                                                                                                                                                                VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                        Houldsworth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88124845; PubMed=2829183;
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Mol. Biol. 206:26
                                                                                                                                                                                                                                                                                                                                        dsworth J., Attardi G.;
distinct genes for ADP/ATP translocase
l in adult human liver.";
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                                                                                                                                                                                                                            PEO PRO-114 AND MET-289
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                                                                                                                                                                                                                                                                                                            Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                    PubMed=10926541;
                                                                                                                                                                                                                                                                                                            Sci.
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EXCHANGE
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Suomalainen
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AND ATP
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                                                                        maintenance.";
                                                                                                                                                Zeviani
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Query Match
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Matches 263; Conser
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CONFLICT
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J03593; AAA36751.1; -. EMBL; J04982; AAA51736.1; -. EMBL; BC008664; AAH08664.1; PIR; A44778; A44778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      REPEAT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRI
PROSITE; PS00215; MITOCH_CARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J02966; AAA61223.1; -.
                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalnoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0006832; P:small molecule transport; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0015207; F:adenine transporter activity; TAS. GO:0006091; P:energy pathways; TAS. GO:0000002; P:mitochondrial genome maintenance; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005887; C:integral to plasma membrane; GO:0005739; C:mitochondrion; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the mitochondrial carrier family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                     μ.
                    I PKEQGVLS FWRGNLANVI RYF PTQALNFA FKDKYKQI FLGGVDKHTQFWRYFAGNLASG
I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                    MTEQAISFAKDFLAGGIAAAISKTAVAFIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family;
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147
227
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                                                                                                                                          Conservative
                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; MITOCH CARRIER; 3.
Inner membrane; Repeat; Transmembrane; Transport;
ly; Disease mutation.
                                                                                                                                                                                                                227
33064
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134
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149
                                                                                                                                                                                                                                                                                                     289
                                                                                                                                                         91.3%;
                                                                                                                                                                                                              MW;
                                                                                                                                        19;
                                                                                                                                      Score 1409; DB 1;
Pred. No. 2.1e-116;
9; Mismatches 16;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowes S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garrier S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Cennicon J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Ra Hostin D., Houston K.A., Howland T.J., Met M., Clabas C.,
Ra Hallah M., Kalush F., Karpen G. H., K. Z., Kennicon J.A., Ketchum K.A.,
Ra Hallah M., Kalush F., Karpen G. H., K. Z., Kennicon J.A., Ketchum K.A.,
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"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";
Experientia 50:749-762(1994).
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STRAIN-Oregon-R;
Zhang Y.Q., Davis A.W.,
Submitted (JAN-1997) to
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Kalush
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Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., A. Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., A. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., A. Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., A. A. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., A. A. Melson L.M., Nelson K.N., Neskern D.E., Moshrefi A., A. Melson D.E., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., A. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier B., Syradling A.C., Stapleton M., Skupski M.P., Smith T., A. Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., A. Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou, Smith H.O., A. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                       EMBL; $43651; AAB23114.1; -.

EMBL; $71762; AAB31734.3; -.

EMBL; $71762; AAB31734.3; -.

EMBL; Y10618; CAA71528.1; -.

EMBL; AE003484; AAF47957.1; -.

EMBL; AV060978; AAL28526.1; -.

EMBL; AV070899; AAL48516.1; -.

EMBL; ACO006839; EMBLOCCHONDITIAL inner membrane; IEI

GO; GO:0006839; F:mitocchondrial transport; IMP.

InterPro; IPR0012067; Mit carrier.

InterPro; IPR001993; Mitoch-Carrier.
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STRAIN=Berkeley; TISSUE=Larva, Ovary, and Pupae;

MEDLINE=22426066; bubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Char

George R.A., Guarin H., Kronmiller B., Pacleb J.M., )

Rubin G.M., Celniker S.E.;

"A Drosophila full-length cDNA resource.";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inner membrane (By similarity).
DOMAIN: Composed of three homologous domains.
SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Catalyzes the exchange of ADP and ATP a mitochondrial inner membrane.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
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7 -> Y (IN REF. 1 AND 2).
7 -> Y (IN REF. 1).
8 -> S (IN REF. 2).
9 -> P (IN REF. 1 AND 2).
9 -> P (IN REF. 1).
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                S (IN REF. 1)
C (IN REF. 2)
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McPherson
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Best Local S
Matches 237
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Q27238;
Q27238;
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Created)
Q27238;
Q27238
             TRANSMEM TRANSMEM TRANSMEM
                                                                                                                                                                                                                     InterPro; IPR002067; Mit carrier.
InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ind
Neoptera; Endopterygota; Diptera; Nematocera.
NCBI TaxID=7165;
                                                                                                                              PROSITE; PS002:
Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L11618; AAB04104.1; EMBL; L11617; AAB04105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94348635; PubMed=8069414; Beard C.B., Crews-Oyen A.B., Kumar V.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRIAL INNER MEMBRANE.
-!- SUBUNIT: Homodimer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: CATALYZES THE EXCHANGE
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    -!- SUBCELLULAR LOCATION: Integral membrane

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J; IPR002.
J; IPR001993; h...
PP00153; mito carr; 3.
S; PR00926; MITOCH CARRIER; 3.
ITE; PS00215; MITOCH CARRIER; 3.
Arion; Inner membrane; Repertance; Repertance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: COMPOSED OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inner membrane
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Pred. No. 7.56
        Repeat; Transmembrane; (POTENTIAL). (POTENTIAL). (POTENTIAL).
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
Chlorella kessleri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilgarth C., Sauer N., Tanner W.,
"Glucose increases the expression of the
glyceraldehyde-1-phosphate dehydrogenase
J. Biol. Chem. 266:24044-24047(1991).
- FUNCTION: CATALYZES THE EXCHANGE OF A
MITOCHONDRIAL INNER MEMBRANE
- I. SUBUNIT: Homodimer (By Similarity).
Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER PROSITE; PS00215; MITOCH_CAR
                                                                  PIR; A41677; A41677.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                           EMBL; M76669; AAA33027.1;
                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92084708; PubMed=1748677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION:
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RESULT 13
ADT3_YEAST
ID ADT3_YEAST
AC P18238;
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TRANSMEM 45
TRANSMEM 108
TRANSMEM 151
TRANSMEM 209
TRANSMEM 248
TRANSMEM 304
TRANSMEM 304
SEQUENCE 339
                                                                                                                                                       Vissers S. Submitted
                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP, ATP carrier protein 3 (ADP/ATP translocase translocator 3) (ANT 3).
AAC3 OR YBR085W OR YBR0753.
                                            Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
Submitted (AUG-1994) to the EWEL/GenBank/DDBJ databases.
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
-MITOCHONDRIAL INNER MEMBRANE.
-I- SUBUNIT: Homodimer.
-I- SUBCELLULAR LOCATION: Integral membrane protein. Mitoch
                                                                                                                                                                                                                           MEDLINE=90324269; PubMed=2165073;
Kolarov J., Kolarova N., Nelson N.;
Kolarov Hernelocator gene i
"A third ADP/ATP translocator gene i
J. Biol. Chem. 265:12711-12716(1990)
                                                                                                                                                                              Andre B.,
                                                                                                                                                                                        STRAIN=S288C
                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                  STRAIN=S288c;
                                                                                                                               SEQUENCE OF 38-307 FROM N.A.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
            DOMAIN: COMPOSED OF SIMILARITY: Belongs
                                     inner membrane
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1 (POTENTIAL).

26 2 (POTENTIAL).

68 3 (POTENTIAL).

8 4 (POTENTIAL).

5 (POTENTIAL).

6 5 (POTENTIAL).
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            THREE HOMOLOGOUS DOMAINS. to the mitochondrial carrier
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6; Mismatches
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RESULT 14

ADT CHIRE
ID ADT C
AC P2700

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Best Local
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                                                                                                                                                                                                                                                                                                                    CHLRE
ADT CHLRE
P27080;
01-AUG-1992
                                                                                                       ABT.
Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M34076; AAA97485.1; -.

EMBL; Z55954; CAA85031.1; -.

PIR; A36582; A36582.

SGD; S0000289; AAC3.

GG; GO:000547; F:ATF/ADP antiporter activity; IMP.

GO; GO:0006864; F:ATF/ADP exchange; IMP.

InterPro; IPR002067; Mit carrier.

InterPro; IPR001993; Mitoch carrier.
                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institute. Institute on restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.i-t-torsend an email to licenseaich
                     SEQUENCE FROM N.A.
STRAIN=FUD44-R2;
MEDLINE=93204887; PubMed=8455552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
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TRANSMEM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCHRERER. PROSITE; PS00215; MITOCH_CARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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J.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVVGIVVYRGLYEGMEDSLKELVLTGSLDGSFLASFLLGWVVTTGASTCSYPLDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMTSGQA---VKYNGAIDCLKKIVASEGVGSLFKGCGANILRSVAGAGVISMYDQLQMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVQGIIIYRAAYFGVYDTAKGM-LPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGALSLLFVYSLDFARTRLAADAKSSKKGGARQFNGLTDVYKKTLKSDGIAGLYRGFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKQEGLISFWRGNTANVIRYFPTQALNFAFKDKIKLMF--GFKKEEGYGKWFAGNLASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQETNFAINFLMGGVSAAIAKTAASPIERVKILIQNQDEMIKQGTLDKKYSGIVDCFKRT
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181
220
276
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                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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96
137
200
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53.7%;
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Pred. No. 4.5e
15; Mismatches
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5e-61;
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                                                                                                                                                                                                                                                                                                                                                              ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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RESULT 15
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AC Q0918
AC Q1-NC
DT 01-NC
DT 28-FE
DE ADP,A
DE trans
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS0021
Mitochondrion;
TRANSMEM 12
TRANSMEM 74
TRANSMEM 116
TRANSMEM 178
TRANSMEM 217
TRANSMEM 273
SEQUENCE 308
ADT_SCHPO STANDARD; PRT; 322 AA (20918); O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) ADP_ATP carrier protein (ADP/ATP translocase translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii."; Mol. Gen. Genet. 237:134-144 (1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00153; mito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X65194; CAA46311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: COMPOSED OF
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157; Conser
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                                                                                                                                                                                                                                                                                              GGAAGAVSLSFVYSLDYARTRLANDAKSAKKGGGDRQFNGLVDVYRKTIASDGIAGLYRG
                                                                                                                                                                     KVI 298
                                                                                                                                                                                                                     RRMMOSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                               FNISCVGIVYYRGLYFGMYDSLKPVVLVGPLANNFLAAFLLGWGITIGAGLASYPIDTIR
                                                                                                                                                                                                                                                                                                                   GGAAGATSLCFVYPLDFARTRLAAD----VGKSGTEREFRGLGDCLVKITKSDGIRGLYQG
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                                                                                                                                                                                                                                                                                                                                                                   RIPKEQGVLSFWRGNLANVIRYPPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00215;
                                                                                                                                                                                                                                                              FSVSVQGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR
                                                                                                                                                                                              RRMMTS--
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74
116
178
178
217
273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCH
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92
133
197
234
291
33528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
             (ADP/ATP translocase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
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7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 772; DB 1; 1
Pred. No. 1.7e-60;
5; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
             (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hormsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
A James K., Jones L., Jones M., Leather S., McDennid S., McLean J.,
RA James K., Jones M., Leather S., McDennid S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDennid S., McLean J.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Gulterford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.,G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.,G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Bord P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Griffeau A., Cochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Garzon A., Thode G.,
RA Certuti G.V., Ussery D., Barrell B.G., Nurse P.
EMBL; Z49974; CAA90275.1; -.
ERBL; AL023634; CAA19176.1; -.
PIR; T40526; T40526.
GeneDB_Spombe; SPBC530.10c; -.
InterPro; IPR00193; mito_carrier.
InterPro; IPR00193; mito_carrier.
Pfam; pF00153; mito_carr; 3.
PRINTS; PR00926; MITOCH CARRIER.
PROSITE; PS00215; MITOCH CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
TRANSMEM 28 48 1 (POTENTIAL).
TRANSMEM 93 111 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=972;
MEDLINE=96257204; PubMed=8675018;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
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음 성	음 성	용 성	음 성	음 성	Z M O	SPITI
. 241 263	182 203	124 143	8 4 8 4	7 26	Query Match Best Local (Matches 158	TRANSMEM TRANSMEM TRANSMEM TRANSMEM SEQUENCE
QSGRKGADIMYTGTVDCWRKIFKDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK :	182 QGIIIYRAAYFGVYDTAKG-MLÞDÞKNTHIVVSWMIAQTVTAVAGVVSYÞÞDTVRRRMM :: : : ; ::: : : 203 VGIVVYRGLYFGMYDTLKÞVVLVGÞLBGNFLASFLLGWAVTTGSGVASYÞLDTIRRRMM	124 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 	64 EQGYLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASGGAA -	7 SPAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK 63 	49.8%; Score 769; DB 1; Length 322; Similarity 53.6%; Pred. No. 3.3e-60; 8; Conservative 50; Mismatches 75; Indels 12;	MEM 131 151 3 (POTENTIAL). MEM 197 217 4 (POTENTIAL). MEM 222 242 5 (POTENTIAL). MEM 289 309 6 (POTENTIAL). MCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;
295 314	RAMAN	SVSV - GPSV	GGAA	RIPK - RTAA	Gaps	
	240	181	123	83 63	٠; و	

Search completed: December 18, Job time : 9.34267 secs 2003, 12:41:25

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
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seq length: 2000000000
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1. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

7. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

7. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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1337.197 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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/SIDS1/gcgdata/genesed/geneseqp-embl/AA1985.DAT: *
/SIDS1/gcgdata/genesed/geneseqp-embl/AA1985.DAT: *
/SIDS1/gcgdata/genesed/geneseqp-embl/AA1986.DAT: *
/SIDS1/gcgdata/genesed/geneseqp-embl/AA1986.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

			ı.			Result
8 1391.5 9 1391.5	6 1398.5 7 1391.5	4 1457.5 5 1442.5	3 1553	2 1553	1 1553	Score
89.6	90.1 89.6	93.9 92.9	100.0	100.0	100.0	Query Match
298 298	298 298	298 293	297	297	297	Query Match Length DB
22 23	23 21	22 22	23	22	21	BB
AAU01199 AAU10379	AA018516 AAY71032	AAW61169 ABU53219	AAU10378	AAU01198	297 . 21 AAY71031	IJ
Human adenine nucl Human adenine nucl	Human insulin rece Human adenine nucl	ANTI protein. Mus . Human metabolism-a	Human adenine nucl	Human adenine nucl	Human adenine nucl	Description

743	743	743	746	746	746	746	746	746	746	746	746	746	746	746	746	746	746	746.5	771	820	867.5	926.5	1101.5	1101.5	1147	1221.5	1241	1241	1268.5	1294.5	•		1385.5		1385.5
47.8	47.8	٠	•	•	•	•	•	•	•	48.0	•	•	•	•	•	•	•	•	•	•	•	•		٠	•	•	•	٠	•	٠	•	•	٠	89.2	•
381	363	346	1027	1009	992	381	381	381	381	363	363	363	363	346	346	346	346	379	301	298	222	228	315	315	307	263	299	299	429	325	323	298	298	298	298
21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	24	23	22	23	23	23	22	22	22	22	22	24	22	22	23	22	22	21
AAG17729	AAG17730	AAG17731	AAG38670	AAG38671	AAG38672	AAG38458	AAG37262	AAG37259	AAG36575	AAG38459	AAG37263	AAG37260	AAG36576	AAG38460	AAG37264	AAG37261	AAG36577	ABP81267	ABP73357	ABG18922	ABP74106	ABP43205	AAE21175	ABU53218	ABB58380	ABG27056	ABB67300	ABB66082	ABR41715	ABG15423	AAM41427	AAU10380	AAU01200	AAM39641	AAY71033
Arabidopsis thalia	Arabidopsis thalia				Arabidopsis thalia	Arabidopsis thalia											Arabidopsis thalia		Candida albicans e	Novel human diagno	TRICH	Human ovarian anti	Human TRICH-19 pro	Human metabolism-a	Drosophila melanog	Novel human diagno	Drosophila melanog	Drosophila melanog		Novel human diagno	Human polypeptide	Human adenine nucl	Human adenine nucl	polypept	Human adenine nucl

ALIGNMENTS

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ARSSULT 1
AAY71031
ID AAY71031
AC AAY7
XX
AC AAY7
XX
DT 29-A
DT 29-A
DT 29-A
XX
Huma
DB Huma
XX
Huma
KW Huma
KW Match
KW Match
KW Match
KW Match
KW Match
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KW Mitch
KW
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Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

WO200026370-A2.

03-NOV-1999; 11-MAY-2000 99WO-US25883.

03-NOV-1998; 08-SEP-1999; 98US-0185904. 99US-0393441.

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RESULT 2
AAUU118
IID AAUU
XX
AC AAUU
XX
DT 07-S
XX
DE Huma
XX
DR Huma
XX
Huma
XX
KW Huma
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KW mitc
XW mitc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MELAS), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an an according translocator ANTI from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                          Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
mitochondrial permeability transition pore component; cell surviva
                                                                                                     Human adenine nucleotide translocator-1 (ANT-1)
                                                                                                                                                07-SEP-2001
                                                                                                                                                                                                                            AAU01198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365619/31.
N-PSDB; AAD00519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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                                                                                                                                                                                                                                                                                                                                SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
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                                                                                                                                                                                                                                                                                                                                                                                                                QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                              Protein;
                                                                                                                                              entry)
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Pred. No. 3.4e-173;
; Mismatches 0;
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                                          survival;
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The present sequence represents human adenine nucleotide translocator-1 (CC (ANT-1) protein. ANT proteins are mitochondrial permeability CC transition (MTP) pore components responsible for mediating transport CC (MTP) pare components responsible for mediating transport CC with other mitochondrial inner membrane. ANT proteins interact CC with other mitochondrial core components e.g. cyclophilins to CC regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel CC components. The methods are useful for screening for agents that alter CC components. The methods are useful for screening for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mentions achievented achievented and achievented achievented and achievented and achievented achievented and achievented and achievented achievented and achievented achievented achievented achievented and achievented achieve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mėllitus, Parkinson's disease, Huntington's disease, schizophrenia,
mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 186pp; English.
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N-PSDB; AAS05901.
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Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-1999;
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                                                                                                                                                                                       QGIIIYRAAYFGVYDTAKGMLÞDÞKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRWMQ 240
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QGIIIYRAAYFGVYDTAKGMLPDFKNVHIFVSMMIAQSVTAVAGLLSYPFDTVRRRMMQ
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                                                                    SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYV
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G, Davis R
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Pred. No. 3.
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3.4e-173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nuclect acid encoding an adenine nuclectide translocator (ANT) polypeptide. ANT contains mediate the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide CC of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide, is CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is covalently or non-CC covalently bound to a solid phase. Detectably labeled ANT ligand is also CC useful for identifying an agent that interacts with an ANT polypeptide. CC The present sequence represents the amino acid sequence of human ANT1.
                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
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N-PSDB; AAS16688.
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                                                                                                                                                                                                                                                                     MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                               I PKEQGELSFWRGNLANVI RYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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100.0%; Pred. No. 3..
tive 0; Mismatches
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MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR

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ARMSULT 4
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                                                                Query Match
                                                                                                                                                                                                                   The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, mypopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antl; Adenine nucleotide translocator; cloning; screening; DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP, ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
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                                                                                                                                                                                        ncrease/mediate ATP and ADP ndependent of ANT1.
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Score 1457.5; DB 1
Pred. No. 5.4e-162;
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                                                                                                                                   Query Match
Best Local S
                                                                                                               Matches
                                                                                                                                                                                                                                                                         This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies -
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28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene'therapy; vaccine; disease treatment; detection.
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                                             AWSPLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKB
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                                                                                                               Conservative
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99US-0156503.
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                                                                                                            Score 1442.5; DB
Pred. No. 3e-160;
0; Mismatches
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12-JAN-2001;
12-JAN-2001;
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12-JAN-2001;
12-JAN-2001;
                                     Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent -
                   Disclosure;
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12-JAN-2001;
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12-JAN-2001;
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12-JAN-2001;
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ISM; diabetes; metabolic syndrome; antidiabetic.
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12-JAN-2001;
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12-JAN-2001;
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                   Page 160-161; 232pp;
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2001US-261589P.
2001US-261590P.
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The present invention relates to

a method

of identifying a candidate

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenine nucleotide translocator ANT2
                                                                             03-NOV-1998;
08-SEP-1999;
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Pred. No. 4.5e-155;
7; Mismatches 15;
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(MITO-) MITOKOR

Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

Human adenine nucleotide translocator-2 (ANT-2) protein.

07-SEP-2001

(first entry)

AAU01199

standard; Protein;

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ARUGIT 8
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AAUGIT AAUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine city of a singular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents cor ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, cacher, shereditary optic neuropathy, schizophrenia, mitochondrial caches and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA;
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7; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention on treatment of diseases associated with altered mitochondrial function or dysfunctional cells survival. These agents are useful for the prevention on dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival. These agents are useful for the prevention or dysfunctional cells survival.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Velicelebi G,
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                                               QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKY 296
                                                                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTVRRRMM 239
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3, Davis RE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1391.5; DB 22;
Pred. No. 3e-154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Ghosh SS, Moos WH,
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                                                                                 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                    I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                            I PKEOEVLSFWRGNLANVIRYFPTOALNFAFKDKYKOI FLGGVDKRTOFWRYFAGNLASG
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Pei Y, Carroll AK;
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Pred. No. 3e-154;
7; Mismatches 16;
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                                                                                    The patent discloses a method to produce adenine nucleotide translocator CC (ANT) proteins or ANT fusion proteins using recombinant expression CC constructs. ANT is a nuclear encoded protein and a major component of constructs and membrane. It mediates transport of adenosine CC di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability CC transition pore, a modulator of apoptosis. ANT is used to identify agents CC or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for CC detect or isolate ANT in a biological sample, and therapeutically for CC and Hunting mitochondrial function, including Alzheimer's, Parkinson's CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic CC epilepsy red ragged fibre syndrome. The present sequence is an CC adentine nucleotide translocator ANT3 from human brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease -
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N-PSDB; AAD00521.
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Ghosh SS;
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08-SEP-1999;
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99US-0393441.
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                                                                         human brain
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Sequence

298

Novel nucleic acids and such as central nervous

polypeptides, useful system injuries -

for

treating

disorders

Example 4;

SEQ ID NO 2786; 10078pp; English

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RESULT 11
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening; arthritis;
                                                                                                                        WPI; 2001-442253/47.
N-PSDB; AAI58797.
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                                                                                                                                                                                              Liu C,
Wang Z,
Zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; canc
                                                                                                                                                      03-NOV-1999;
                                                                                                                                                                                                                           03-NOV-2000; 2000WO-US30535
                                                                                                                                                                                                                                                                                                     10-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
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Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                  99US-0434354
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Pred. No. 1.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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les 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  survival;
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Murphy AN,

Clevenger W,

Wiley SE,

Andreyev AY,

Frigeri

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Homo sapiens mitochondrial AAU10380;

14-FEB-2002

(first entry

Human adenine nucleotide translocator 3

(ANT3).

adenine nucleotide translocator;

matrix

protein

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RESULT 13
AAU10380
ID AAU10
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AC AAU10
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AC AAU10
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TI4-FE
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DE Human
XX
KW Human
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KW mitoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MT) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid
                                                                                                                                                                                                           AAU10380 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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                                                                                                                                                                                                                                                                                                       QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                                                                         VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTEQAISFAKDFLAGGIAAAISKTAVAPIBRVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 2, 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                           Protein; 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT 14
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AC AAM41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest.

CC useful for identifying an agent that binds to an ANT polypeptide. ANT culgand is useful for determining the presence of an ANT polypeptide. Preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating the presence of a covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
 AAM41427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                 AAM41427 standard; Protein; 323 AA
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                                                                                                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                                                                                       MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                    MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                      QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                               VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                     IPKEQGELSFWRGNLANVIRYEPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                  OSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                     I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M, Davis
Moos WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RB, Clevenger W, W
Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1385.5; DB 23; Length Pred. No. 1.5e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for producing adenine nucleotide regulated promoter linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, commonsuppressant and cytostatic activity. The polynuclectides are useful CC in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous gystem, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, arthritis and inflammation, leukaemias and CC N.S disorders.

CC N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
                                                                                  Matches
                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                        Sequence
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Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
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19-OCT-2000;
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                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; SEQ ID NO 6358; 10078pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z,
Zhou P,
                       MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations (II) considered to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 45782; 103pp; English
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23-AUG-2000; 2000US-0649167.
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                                                              MMOSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYD-EIKK
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 US-08-961-871-10
US-09-434-354-48
US-09-434-354-29
US-09-96-243-289
US-09-96-243-289
US-09-96-119-2
US-09-160-119-2
US-09-160-119-2
US-09-160-119-2
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Sequence 47, Appl
Sequence 48, Appl
Sequence 49, Appl
Sequence 39, App
Sequence 339, App
Sequence 339, App
Sequence 2, Appli
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Sequence 118, App
Sequence 118, App
Sequence 12, Appli
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			Query l Best Lo Matcher	RESULT 1 Sequence 47, Patent No. GENERAL INF APPLICANT: APPLICANT		00010000000000000000000000000000000000
241 S 241 S	121 0	61 I 61 I 81 I	70	SULT 1 -09-434-354-47 Sequence 47, Appled Figure 10. 6562 GENERAL INFORMAN APPLICANT: Mult APPLICANT: Will APPLICANT: Will APPLICANT: WILL APPLICANT: UNTITLE OF INVENTITLE OF SUCCEPTARE FEBELS CURRENT FILING CUR		222.5 218.5 218.5 218.5 218.5 218.5 208.5 1196.5 1196.5 1196.5 1192 1192 1192 1192 1192 1192 1192 119
SGRKGADIMYTGTVDCWRKIAKDEGAKAF 	GAAGATSLCFYYPLDFARTRLAADVGRAAQREFEGLGDCIIKIFKSDGLRGLYQGFNVSV	ngdhamsplkdflagavaaavsktavapiervklllqvqhaskqisaekqykgiidcvvr PKEQGFLSFWRGNLANVIRyffTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 	100.0%; Score 1553; DB 4; Length 297; Similarity 100.0%; Pred. No. 4.2e-172; 7; Conservative 0; Mismatches 0; Indels 0; Gaps MGDHAWSFLXDFLAGAVAAAVSKTAVAPIERVKLLLOVOHASKQISAEKQYKGIIDCVVR	jlica FION: FION: FION: Jeri, Jeri, Jerion: FION		11111111111111111111111111111111111111
TGTVDCI	EGAZDII	DFLAGA	100.	Anne N. Anne N. Ir, William r., Allean sileen Alexander Y. Luciano G. bi, Gonul cobert E. COMPOSITIONS AND N. INTERACTIONS OF M. IDENTIFYING AGENTS 1088.433 INUMBER: US/09/434. 1199-11-03 S: 54 Or Windows Version ien		30033 3003 3003 3003 3003 3003 3003 30
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A.C.D.E.C.	LAAD	VSKTI	Score Pred. ; Mism VSKTAV!	9434354 m een err. G. IONS AND ME IONS OF MIT ING AGENTS US/09/434,3 -03 8 Version 3	Ž.	US-09- US-09- US-09- US-09- US-09- US-09- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-09- US-08- US
SAKAI	ONVHI	DALMI DALMI DALMI	ore 15 ed. No Mismat	MIRON METERS 134,315	ALIGNMENTS	9-503-579-2 9-37-466-4 9-172-528-4 9-138-19-4 9-503-579-4 9-501-558-4 9-501-681A-5 9-210-681A-5 9-46-719A-5 9-547-983-56 8-470-861A-3 8-807-861A-3 8-807-861A-3 8-807-861A-3 9-246-719A-3 9-246-719A-3 9-547-983-3-1
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PKGAMSNVLRGMGGAFVLVLYDEIKKYV PKGAMSNVLRGMGGAFVLVLYDEIKKYV	SVTAN	DLFLGC	4; I 172; 0; I	FOR DETERMINING DRIAL COMPONENTS, AND F ALTER SUCH INTERACTIONS		
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US-08-961-871-10
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US-08-961-871-10
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                           Matches 279; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,871 FILING DATE: 31-OCT-1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA: 800 PRIOR APPLICATION US 60/030,017 FILING DATE: 01-NOV-1996 ATTORNEY/AGENT INFORMATION: NAME: VERSION US 60/030,017 PILING DATE: 01-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OP INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OP INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                    QSGRKGADIMYTGTVDCWRKIAKDBGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYV 297
                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
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    OSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
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5370 Manhattan Circle, Suite 201
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US-09-434-354-48

RESULT 3

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APPLICANT: Murphy, Anne N.
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Davis, Robert B.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
LERNOTH: 298
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APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert B.
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; ORGANISM: Homo mapien
US-09-434-354-48
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TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FO
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 48
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/09434354 Patent No. 6562563
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Patent No. 6562563
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Best Local Similarity
ORGANISM: Homo sapien
                                              ENGTH:
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RESULT 5
US-09-996-243-289
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                                                             CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR TILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065111
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
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Matches
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                                                                                                                                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
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OR APPLICATION NUMBER: 60/049787
OR FILING DATE: 1997-06-16
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
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Baker, Kevin P.
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Williams, P. Mickey
Wood, William I.
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art, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                              Nicholas F.
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87.2%; Pred. No. 1.3e-152;
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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19

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APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

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APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801

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FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600

FILING DATE: 1998-06-17

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steaman, Matthew
APPLICANT: Onrust, Ranthew
APPLICANT: Onrust, Rane
APPLICANT: Onrust, Rane
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: and Methods For Their Use
TITLE OF INVENTION: and Methods For Their Use
TILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
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PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
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Patent No. 61505
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62 PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYFAGN 116 : | : | : | : | : | : | ::
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29.0%; Pred. No. 1.4e-26;
                                                                                                                                             ; Score 301; DB 3; Length 46; Pred. No. 3e-26; 64; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Mismatches
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519

1998-07-02

FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478

FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360

PILING DATE: 1998-00
APPLICATION NUMBER:

1998-06-26

60/090863

APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-25 FILING DATE: 1998-06-25

APPLICATION NUMBER:

60/090696

APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695

APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690

FILING DATE: 1998-06-25

FILING DATE: 1998-06-25

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676

PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542

APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535

PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252

FILING DATE: 1998-06-19 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/089948

FILING DATE: 1998-06-22

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
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ORGANISM: Mouse
-09-312-283C-339
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TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000:1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
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454
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                                                                                                                                                                                                                                                                                                                                                   62 PKBQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYFAGN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
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                                      LVLYDEIK 294
                                                                                                               YPFDTVRRRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFV- 286
                                                                                                                                                     IPNMLGIIPYAGIDLAVYETLKNTWLQRYAVNSADP---GVFV-LLACGTISSTCGQLAS
                                                                                                                                                                                           NVSVQGIIIYRAAYFGVYDTAKGM-----LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227
                                                                                                                                                                                                                                                                                                              IREGGAKSLWRGNGINVLKIAPESAIKFMAYEQMKRLV--GSDQETLRIHER-----
                                                                                                                                                                                                                                                                                                                                                                                         WRHL---VAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM------CIVGGFTQM 233
                                                                                                                                                                                                                                                                                                                                                                                                                               WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVV----RI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPLALVRTRMQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSIS 453
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YVVYENLK 461
                                                                                                                                                                                                                                LVAGSLAGATAOSSIYPMEVLKTRMAL----RKTGOYSGMLDCARRILAKEGVAAFYKGY 339
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                                                                          YPLALVRTRMQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSIS 453
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Sleeman, Matthew
Onrust, Rene
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28.9%; Pred. No. 3e-26;
tive 64; Mismatches 103; Indels
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                                                                                                   FITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-160-119-2
                                                      SOFTWARE: Fab., SEQ ID NO 2 FORGTH: 674
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09160119A Patent No. 6316219
GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                         APPLICANT: KRIEF, STEPHANE APPLICANT: SOUCHET, MICHEL APPLICANT: BRIL, ANTOINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/160,119A CURRENT FILING DATE: 1998-09-24 EARLIER APPLICATION NUMBER: EP 97402511.6 EARLIER FILING DATE: 1997-10-23 EARLIER APPLICATION NUMBER: EP 98401655.0 EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4
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                  LENGTH: 674
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIKTR--LQVAARAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLLPQLLGVAPEKAIKLTVNDFVRDKFM-----HKDGSVPLAAEILAGGCAGGSQVIFT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCFV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGLGSVAGAVGATAVYPIDLVKTRMONORSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 163
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27.5%;
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Pred. No. 4.1e-25;
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RESULT

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH; 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-501-558-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0012-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497
                                     242 G-RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDBIKK 295
                                                                                 178 VELPVYDITKKHLILSGLMGDTVYTHFLSSF----TCGLAGALASNPVDVVRTRWMNOR
                                                                                                                                                                   122 TIANPTDVLKIRMQA----QSNTIQGGMIGNFMNIYQQEGTRGLWKGVSLTAQRAAIVVG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYPFDTVRRRMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446 NPLEIVKIRLQVÄGEITTGPRVS------ALSVVRDLGFFGIYKGAKACFLRDIPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 YPLDFARTRL--AADV--GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
233
                                                                                                                                                                                                               129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2, Application US/09501558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 RGLLPQLLGVAPEKAIKLTVNDFVRDKFM-----HKDGSVPLAAEILAGGCAGGSQVIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 FGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
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                                                                                                                                                                                                                                                         67 ALYSGIAPAMLROASYGTIKIGTYOSLKRLF---IERPED--ETLPINVICGILSGVISS
                                                                                                                                                                                                                                                                                                 69 SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                10 KDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQIS-ABKQYKGIIDCVVRIPKEQGFL 68
                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | CTTYSGVIDCERKILREEGPKALMKGAGARVERSSPQEGVTLLTYELLQRW 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGG-AFVLVLYDEIKKY 296
  VLRDGRCSGYTGTLDCLLQTWKNEGFFALYKGFWPNWLRLGPWNIIFFVTYEQLKK 288
                                                                                                                         AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAG-LLSYPFDTVRRRMMQS 241
                                                                                                                                                                                                                                                                                                                                           KPFVYGGLASITAECGTFPIDLTKTRLÓIQGQTNDAKFKEIRYRGMLHALVRIGREEGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIYPPCYAHVKASPANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIKTR--LQVAARAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGFLSFW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sands, Arthur T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turner, C. Alexander Jr. Mathur, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zambrowicz, Brian
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28.4%;
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53; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 267; DB 4;
Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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Best Local Similarity
Thes 89; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/092,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (335)
OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 335
                                                                                                                                      187
                                                                                                                                                                                                                                   127
                                                                                          220 VGVELPVYDITKKHLILSGMMGDTILTH-----FVSSFTCGLAGALASNPVDVVRTRMMN
                                                                                                                                                                                       164 SSTIANPTDVLKIRMQAQ-GSLFQGSMIG---SFIDIYQQEGTRGLWRGVVPTAQRAAIV 219
275 QRAIVGHVDLYKGTVDGILKMWKHEGFFÁLYKGFWPNWLRLGPWNIIFFITYEQLKR 331
                                                                                                                                                                                                                                                                               109 VLALYSGIAPALLKQASYGTIKIGIYQSLKRLF---VERLED--ETLLINMICGVVSGVI 163
                                                                                                                                                                                                                                                                                                                                67 FLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGAT 126
                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                        10 KDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA---EKQYKGIIDCVVRIPKEQG 66
                                                                                                                                      RAAYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAG-LLSYPFDTVRRRMMM 239
                                                                                                                                                                                                                                      SLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIY 186
                                         QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GWGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                                                                                                                                                                            KPFVYGGLASIVAEFGTFPVDLTKTRLQVQ--GQSIDARFKEIKYRGMFHALFRICKEEG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.1%; Score 265.5; DB 4; 30.0%; Pred. No. 2.4e-22; rative 43; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                               274
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US-08-933-750C-12 RESULT 12 Sequence 12, Appl Patent No. 593244 GENERAL INFORMATION: APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES APPLICANT: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: APPLICANT: APPLICANT: APPLICANT: APPLICANT: STREET: 3174 Por CITY: Palo Alto ADDRESSEE: Application US/08933750C 3: Incyte Pharmaceuticals, Au-Young, Janice Yue, Henry Lal, Preeti Hillman, Jennifer L. Bandman, Olga Shah, Purvi

RESULT 11 US-09-482-273-118

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

IBM Compatible Diskette COUNTRY: USA

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                                                                                                          Sequence 12, Apparent No. 613
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                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: SPLNN
CLONE: 207452
                                                         APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                      APPLICANT:
                                         APPLICANT:
                                                                          APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
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                                                                                                                                                                                                                       303
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                                                                                                                                                                                                                                                                                               243
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                                                                                                                                                                                                                                                                                                                                                                                                         191 FGVYDTAKGMLPDPKNVHIFVSWMI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 VYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAAY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LAGAVAAAVSKTAVAPIERVKLLLQVQHAS-KQISAEKQYKGIIDCVVRIPKEQGFLSFW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 15.3%;
Similarity 23.5%;
                                                                                                                                                                                                                       YE 304
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                                                                                                                                                                                                                                                           YD 291
                                                                                                                                                                                                                                                                                               RLQVGGFEHARAAFGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFMFFS
                                                                                                                                                                                                                                                                                                                                 RMMM---QSGRK--GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                          VHPVDVLRTRFAA---QGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAPTLIAIFPYAGLQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQEEGPTAFW 79
                                                                                                                                                                                                                                                                                                                                                                     FSCYSSLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
                                                                                                              Application US/09234613
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                              Lal, Preeti
Hillman, Jennifer
Bandman, Olga
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Au-Young, Janice
                    Shah,
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                 Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Mismatches 124; Indels
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Pred. No. 3.6e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                      ----AQSVTAVAGLLSYPFDTVRR 235
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RESULT 14 US-09-142-565-2

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/ CLONE: 2
US-09-234-613-12
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SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,
FILING DATE: September 23, 19;
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
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MEDIUM TYPE: Diskette
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APPLICANT: Corley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: Sr. 207452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 23.5 les 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                      290
                                                                            243
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                                                                                                                                                                                                                                                                                                                                                                                      20 VAGSVSGLVTRALISPEDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQBEGFTAFW
                                                                                                                                                                                                                                                                                                                                                72 RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCF 130
                                                                                                                                                                                                                                                                                                                                                                                                                            13 LAGAVAAAVSKTAVAPIERVKLLLQVQHAS-KQISAEKQYKGIIDCVVRIPKEQGFLSFW 71
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                                                                                                                                                                                                                                                                     VYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAAY 190
                                      YD 291
                                                                            RLQVGGFEHARAAFGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFMFFS 302
                                                                                                              RMMM---QSGRK--GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVL 289
                                                                                                                                                                                                                                 VHPVDVLRTRFAA---QGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAPTLIAIFPYAGLQ 192
                                                                                                                                                                                                                                                                                                           KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
YE 304
                                                                                                                                                  FSCYSSLK-----HLY-KWAIPAEGKKNENLQNLLCGSGAGVISKTLTYPLDLFKK
                                                                                                                                                                                           FGVYDTAKGMLPDPKNVHIFVSWMI - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLINOT02
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RESULT 15
US-08-518-878B-56
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56, Application US/08518878B Patent No. 5702902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.0%; Score 233.5; DB 3; Best Local Similarity 24.7%; Pred. No. 1.2e-18; Matches 73; Conservative 53; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: HOMO SAPIEN
-09-142-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENERAL
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APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GH-30002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/518,878B
                                                                               ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: F1Oppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 312
                                                                                                                                                                                                                                                                                                                            APPLICANT: Tartagli
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                   STATE: New York COUNTRY: U.S.A.
  FILING DATE:
                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                       DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 VNCAEVVTYDILKEKLLD---YHLLTDNFPCHFVSAFGAGFCATVVASFVDVVKTRYM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ---NSPPGQYFSPLDCMIKMVAQEGPTÄFYKGFTPSFLRLGSWNVVMFVTYEQLKR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 YRAAYFGVYDTAKGMLEDPKNVHIFVSWMIAQSVTA----VAGLLSYPFDTVRRRMMMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 TCAQPTDVVKVRFQASIHLGPSRSDRKYSGTMDAYRTIARBEGVRGLWKGTLPNIMRNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 CFVYPLDFARTRLAADV---GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/142,565A
FILING DATE: 1999-06-30
APPLICATION NUMBER: 9704551.2
FILING DATE: 1997-03-05

    Application US/09142565A
    6187560

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEK--QYKGIIDCVVRIPKEQGFLS
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                                                                                                                                                                                                                                                 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                         Tartaglia,
                                                                                                                                                                                                                                                 Pennie & Edmonds
55 Avenue of the Americas
23-AUG-1995
                                                                                                                                                                                                                                                                                                                                COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                                                                                                                                                         Louis A.
                   US/08/518,878B
                                                              #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.6%;
Best Local Similarity 23.8%;
Matches 70; Conservative 5
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                    182 AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM----
                                                                                                                              189
                                                                                                                                                                      122 AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC 181
234 -NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR
                                   243 RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                                           129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
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                                                                                                                                                                                                                                                                                                                                          FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 66
                                                                                                                         AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSG 242
                                                                                                                                                                                                                                                        SLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHAS----IGSRLLAGSTTGALAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56:
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    286
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Search completed: December 18, 2003, 12:44:54 Job time : 13.3057 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
/ Cgm2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
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6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                            NEW_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	query Query Match Length DB	DB	ID .	Description
1	1553	100.0	297	9 !	US-09-811-094-31	Sequence 31, Appl
N	1553	100.0	297	9	US-09-810-644-31	Sequence 31, Appl
w	1553	100.0	297	10	US-09-185-904A-31	Sequence 31, Appl
4	1391.5	89.6	298	9	US-09-811-094-32	Sequence 32, Appl
_U	1391.5	89.6	298	9	US-09-810-644-32	Sequence 32, Appl
0	1391.5	89.6	298	10	US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.2	298	ø	US-09-811-094-33	Sequence 33, Appl
8	1385.5	89.2	298	ø	US-09-810-644-33	Sequence 33, Appl
9	1385.5	89.2	298	10	US-09-185-904A-33	Sequence 33, Appl
10	773.5	49.8	179		US-10-029-386-32501	Sequence 32501, A
11	771	49.6	301	12	US-10-032-585-7194	Sequence 7194, Ap
12	740	47.6	381		US-10-141-478A-2	Sequence 2, Appli
13	734	47.3	318	10	US-09-801-368-252	Sequence 252, App
14	734	47.3	386	9	US-09-734-569-170	Sequence 170, App
15	703.5	45.3	308	15	US-10-128-714-3338	Sequence 3338, Ap

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
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CURRENT APPLICATION NUMBER: US/09/811,094; CURRENT FILING DATE: 2001-03-14; NUMBER OF SEQ ID NOS: 37; SOPTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 31; LENGTH: 297; TYPE : PRT; ORGANISM: Homo sapien
US-09-811-094-31
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Patent No. US20010044144A1
                                                                                                                                       Matches 297;
                                                                                                                                                       Query Match 100.0%; Score 1553; DB 9; Best Local Similarity 100.0%; Pred. No. 2.3e-160;
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                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D4
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61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                           1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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Willer, Scott W.
Szabo, Tomas R.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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US-09-810-644-31
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
S-09-810-644-31
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APPLICANT: Davis, Rob
APPLICANT: Clevenger,
APPLICANT: Wiley, San
APPLICANT: Willer, So
APPLICANT: Szabo, Tom
APPLICANT: Ghosh, Sou
APPLICANT: Moos, Walt
APPLICANT: Pei, Yazho
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Best Local Similarity
Matches 297; Conserv
                                  GENERAL INFORMATION:
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Clevenger, William
Wiley, Sandra Elleen
Wiler, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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                                                                                                                                                                   Anderson, Christen M. Davis, Robert E.
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100.0%; Pred. No. 2.3e-160;
ative 0; Mismatches 0;
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
ITILE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND TITLE OF INVENTION: THEREFOR (ANT), NOVEL ANT LIGANDS AND CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FLING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-31
100.0%; Score 1553; DB 10; Length 100-185-904A-31
                                                                  ; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo 8
US-09-811-094-32
                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiler, Scott W.
APPLICANT: Scabb, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
APPLICANT: Pei, Yazhong
APPLICANT: Pei, Yazhong
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US-09-811-094-32
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
SEQ ID NO 32
Query Match
Best Local Similarity
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  89.6%;
  Score 1391.5; DB 9;
Pred. No. 8.3e-143;
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US-09-810-644-32
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                                                                                                                                                                                                                                                                                                                                                              Query Match 89.6%; Score 1391.5; DB 9; Best Local Similarity 88.6%; Pred. No. 8.3e-143; Matches 263; Conservative 17; Mismatches 16;
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LENGTH: 298
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOPTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapien
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Clevenger, William
Wiley, Sandra Bileen
Willer, Scott W.
Szabo, Tomas R.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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                   QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 296
                                                                                                                                         GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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US-09-185-904A-32
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09811094 Patent No. US20010044144A1
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Best Local Similarity 88.6%;
Matches 263; Conservative 1
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AN TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT APPLICATION UNDERS: 37
                                                                                                                                                                                                                                                 APPLICANT: Anderson, Christen M. APPLICANT: Davis, Robert E. APPLICANT: Clevenger, William
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LICTURE OF INVENTION: THEREPOR
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pred. No. 8.3e-143;
Pred. No. 8.3e-16; II
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US-09-810-644-33
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, Willian
APPLICANT: Wiley, Sandra Eila
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
                                                                                                                                                                                        Query Match 89.2%; Score 1385.5; DB 9
Best Local Similarity 87.2%; Pred. No. 3.7e-142;
Matches 260; Conservative 21; Mismatches 16;
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Patent No. US20020012992A1
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                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
-09-810-644-33
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121 GAAGATSLCFVYFLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
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Wiley, Sandra Elleen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Sounitra S.
Moos, Walter H.
Pei, Yazhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I PKEQGVLS FWRGNLANVIRY FETQALNEA FKDKYKQI FLGGVDKHTQFWRY FAGNLASG
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                                                                                                                                                                                                                            DB 9;
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US-10-029-386-32501
US-10-029-386-32501
; Sequence 32501, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 260; Conserv
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APPLICANT:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LITTLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                            241
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
                                                                                                                                                                                                                                                                         QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                       VQGIIIYRAAYEGVYDTAKGMLEDEKNVHIEVSWMIAQSVTAVAGLLSYEEDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                    GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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FILE REFERENCE: AEOMICA-X-2

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; SEQ ID NO 7194
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7194
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US-10-032-585-7194
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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LENGTH: 179
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
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NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 49.8%; Score 773.5; Local Similarity 88.3%; Pred. No. 6.7e es 144; Conservative 12; Mismatches
  183
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                                                                          TSLCFVYPLDFARTRLAADVGRR----AQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQG 182
                                                                                                                                      GFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                           NFFVDFMMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKQGRLEKRYTGIVDCFKRTAADE
                                                                                                                                                                                                                  SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ 65
IIIYRAAYFGVYDTAKG-MLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQS 241
                                                                                                                 GVVSFWRGNTANVIRYFPTQALNFAFKDKFKAMF--GFKKDENYWKWFAGNLASGGLAGA
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                                   TSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGFGPSVIG 182
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EXPRESSED IN LUNG, SIGNAL = 1.2

EXPRESSED IN HELA, SIGNAL = 3.5

EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

EXPRESSED IN BRAIN, SIGNAL = 0.95

EXPRESSED IN BONE MARROW, SIGNAL = 0.96

EXPRESSED IN BONE MARROW, SIGNAL = 0.96

EXPRESSED IN BONE MARROW, SIGNAL = 0.96
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Pred. No. 2.5e-75;
43; Mismatches 82
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                                                                                                                                                                                                                                                                                                               Length 301;
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RESULT 13 US-09-801-368-252

GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian

Robert

APPLICANT:

Hecht, Peter Holtzman, Dou

Sequence 252, Application US/09801368 Patent No. US20020128250A1
GENERAL INFORMATION:

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US-10-141-478A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,527
PRIOR FILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Voelker, Toni
APPLICANT: Zang, Wei
TITLE OF INVENTION: Metabolite Transporters
FILE REFERENCE: 16515.146
CURRENT APPLICATION NUMBER: US/10/141,478A
CURRENT FILING DATE: 2002-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Valentin, Henry APPLICANT: Savage, Thomas APPLICANT: Voelker, Toni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
369
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                                                                                                                                                                                              180 VQGIIIYRAAYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVR 234
                                                                                                                                                                                                                                                                                                                       137 DEGFGSLWRGNTANVIRYFFTQALNFAFKDYFKRLFNFKKDR-DGYWKWFAGNLASGGAA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165;
                                                                                                                                                                                                                                                                                                                                                   64 EQGELSFWRGNLANVIRYFFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                     79 NFALDFLMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIKAGRLSEPYKGIGDCFGRTIK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn version 3.0
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LIVEGKKY 376
                                                                                                                 RRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEI- 293
                                                                                                                                                        CVGIIVYRGLYFGLYDSVKPVLLTGDLQD----SFFASFALGWVITNGAGLASYPIDTVR
                                                                                                                                                                                                                                        GASSLLFVYSLDYARTRLANDAKAAKKGGGGRQFDGLVDVYRKTLKTDGIAGLYRGFNIS 255
                                                                                                                                                                                                                                                                           GATSLCFVYPLDFARTRLAADVGRRAQ----REFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KXY 296
                                                                           RRMMMTSNEA---VKYKSSLDAFKQILKNEGAKSLFKGAGANILRAVAGAGVLSGYDKLT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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Pred. No. 8.1e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 381;
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US-09-734-569-170
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LENGTH: 318
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                          Sequence 170, Application US/09734569
Patent No. US20020064816A1
                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                APPLICANT: Lerchl, Jens
APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
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APPLICANT:
TITLE OF INVENTION: Moss genes from Physcomitrella patens TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAS-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILLING DATE: 2001-03-07
CURRENT FILLING DATE: 2001-03-07
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOA---VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVVYRGLYFGMYDSLKPLLLTGSLEGSFLASFLLGWVVTTGASTCSYPLDTVRRRMMTS
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                                                                                                                        Freund, Annette
Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
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                                                                                                                                                                                                  Frank, Markus
                                                                                                                                                                                                                     Bischoff, Friedrich
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Pred. No. 2.8e-71;
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                                                                                                       encoding proteins involved
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7 SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA---EKQYKGIIDCVVRIPK 63

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US-10-128-714-3338
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US-10-128-714-3338
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                                                                                                                                                                                                                                                                          FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 170
LENGTH: 386
  Best Local Similarity Matches 150; Conserv
                                                                                                                                                              SOPTWARE: PatentIn version 3.1
SEQ ID NO 3338
LENGTH: 308
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Best Local Similarity 52.9%;
Matches 156; Conservative 43
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                                           Query Match
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                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Methods of Use
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                                                                                                         TYPE: PRT ORGANISM: Aspergillus fumigatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 TŚGEA---VKYNGSMDAFKQILAKEGAKSLFKGAGANILRAVAGAGVLSGYDQLQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 ASSLLFVYSLDYARTRLANDAKSSKKGGGERQFNGLVDVYKKTLATDGIAGLYRGFAISC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hu, Wengi
Tishkoff, Daniel
Zamudio, Carlos
Broshkin, Alexey M
Lemieux, Sebastien M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
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45.3%; Score 703.5; DB 15, 50.8%; Pred. No. 5.7e-68; ive 45; Mismatches 87;
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                                               DB 15;
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       Indels
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       13;
       Gaps
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γ	64 EQGELSFWRGNLANVIRYFETQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAA 123	
Db	65 AEGVMSLWRGNTANVIRYPPTQALNPAFRDTYKSMPAYKKDR-DGYAKWMMGNLASGGAA 123	
Qγ	124 GATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180	
Db	124 GATSLLEVYSLDYARTRLANDAKSAKGGGERQFNGLIDVYRKTLASDGIAGLYRGFGPSV 183	
Qγ	181 QGIIIYRAAYEGVYDTAKG-MLEDEKNVHIFVSWMIAQSVTAVAGLLSYEEDTVRRRMM 239	
Db	184 LGIVVYRGLYFGMYDSIKÞVVLVGSLEGSFLASFLLGMTVTTGAGIASYPLDTIRRRMM 243	
Ş	240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAMSNVLRGWGGAFVLVLYDEIK 294	
υ	244 TSGEAVKYKSSLDAARQIIAKEGVKSLFKGAGANILRGVAGAGVLSIYDQVQ 295	
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Post-processing: Minimum Match 0%
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1: pir1:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                        283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                1 MGDHAWSFLKDFLAGAVAAA.....LRGMGGAFVLVLYDBIKKYV 297
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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carrier	ATP carrier	carrier	ADP, ATP carrier pr	carri	tical pro	ATP	carrier	ATP carrier		transloc	carrier	carri	tical pro	carrier p	·i.	-			hypothetical prote	carrier	ATP	carrier	carrier	carrier	carrier		adenine nucleotide	ADD, ATP_carrier pr	tion	

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327	34.5	45.5	349.5	50.5	363	67.5	368	508	676	18.5	28.5	729	33.5	734	736
21.1	21.5	22.2	22.5	22.6	23.4	23.7	23.7	32.7	43.5	46.3	46.9	46.9	47.2	47.3	47.4
332	348	358	352	475	381	325	415	327	298	309	306	305	313	318	307
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T47703	D84798	T45934	T01729	T50686	T51158	T04273	T48171	T51577	T24029	A24849	T42011	S68154	XWNC	A31978	A36582
Ca-dependent solut	probable mitochond	hypothetical prote	mitochondrial solu		 hypothetical prote 	hypothetical prote	hypothetical prote	ADP/ATP translocas	hypothetical prote	ADP, ATP carrier pr					

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A;Experimental source: liver C;Genetics: A;Genetics: A;Gene: GDB:ANT; T1 A;Cross-references: GDB:119680; OMIM:103220 A;Map position: 4q35-4q35 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <amt> F;2-99/Domain: ADP,ATP carrier protein repeat homology <acp1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <acp2></acp2></acp1></amt>	A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-15,'A',17-146,'RR',149,151-226,'L',228-298 <nrc 1-37="" 1988="" 377-381,="" 85,="" <-hous="" a28116="" a94197;="" a;accession:="" a;cross-references:="" a;experimental="" a;molecule="" a;reference="" a;residues:="" a;title:="" acad.="" adp="" are="" atp="" attardi,="" clone="" distinct="" expre="" for="" g.="" gb:j02966;="" gb:j03593;="" genes="" j;="" mrna="" muid:88124845;="" natl.="" nid:c3339724;="" nid:g339919;="" number:="" phmant="" pidn:aaa36751.1;<="" pidn:aaa61223.1;="" pmid:2829183="" proc.="" r;houldsworth,="" sci.="" source:="" th="" translocase="" two="" type:="" u.s.a.=""><th>A; Accession: S03893 A; Status: not compared with conceptual translation A; Status: not compared A; Molecule type: DNA A; Residues: 1-298 <coz> R; Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace R; Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace R; Title: cDNA sequence of a human skeletal muscle ADP/ATP A; Title: cDNA sequence of a human skeletal muscle ADP/ATP A; Reference number: A39891; MUID:88041149; PMID:2823266 A; Accession: A39891</coz></th><th>tein T1 - human mitochondrial ADP iens (man) #sequence revisi. \$03893; \overline{A39891;} \$03893; \overline{A39891;} \$03893; \overline{A39891;} \$1398-14004, 198 scie adenine nucl. A44778; MUID:893 ry ALA LIA LIA LIA LIA LIA CB:J04982; NID:9 Swick, M.J.; Walk /th><th>37 508 32.7 327 2 T5.577 38 368 23.7 415 2 T48171 39 367.5 23.7 325 2 T04273 40 363 23.4 381 2 T51158 41 350.5 22.6 475 2 T05686 42 349.5 22.5 352 2 T01729 43 345.5 22.2 358 2 T45934 44 334.5 21.5 348 2 D84798 45 327 21.1 332 2 T47703 ALIGNMENTS</th></nrc>	A; Accession: S03893 A; Status: not compared with conceptual translation A; Status: not compared A; Molecule type: DNA A; Residues: 1-298 <coz> R; Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace R; Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace R; Title: cDNA sequence of a human skeletal muscle ADP/ATP A; Title: cDNA sequence of a human skeletal muscle ADP/ATP A; Reference number: A39891; MUID:88041149; PMID:2823266 A; Accession: A39891</coz>	tein T1 - human mitochondrial ADP iens (man) #sequence revisi. \$03893; \overline{A39891;} \$03893; \overline{A39891;} \$03893; \overline{A39891;} \$1398-14004, 198 scie adenine nucl. A44778; MUID:893 ry ALA LIA LIA LIA LIA LIA CB:J04982; NID:9 Swick, M.J.; Walk	37 508 32.7 327 2 T5.577 38 368 23.7 415 2 T48171 39 367.5 23.7 325 2 T04273 40 363 23.4 381 2 T51158 41 350.5 22.6 475 2 T05686 42 349.5 22.5 352 2 T01729 43 345.5 22.2 358 2 T45934 44 334.5 21.5 348 2 D84798 45 327 21.1 332 2 T47703 ALIGNMENTS
carrier protein repeat homology n; transmembrane protein predicted <mat> mology <acp1> homology <acp2></acp2></acp1></mat>	26,'I',228-298 <nec>; PIDN:AAA61223.1; PID:g339920 1988 anslocase are expressed at the mRNA level in acpmid:2829183 PMID:2829183</nec>	tion R., Wallace, D.C. 987 21e ADP/ATP translocator: lack of a leader D:2823266	,ATP translocase 1 on 17-Mar-2000 #text_change 17-Mar-2000 A28116 Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M. cotide translocator gene has four exons, is located 40499; pMID:2547778 178658; PIDN:AAA51736.1; PID:g178659 er, J.E. sed nuclear genes for human mitochondrial ADP/ATP tx. 36396; PMID:2541251	ADP/ATP translocas hypothetical prote hypothetical prote hypothetical prote peroxisomal Ca-dep mitochondrial solu hypothetical prote probable mitochond Ca-dependent solut

20-Aug-1999

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C;Accession: I60173
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of cDNA clones and A;Reference number: 160173; MUID:94002161; PMID:8399300
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
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9; Mismatches 7;
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2; Mismatches 2;
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S37210
ADP,ATP carrier protein T1 - mouse
ADP,ATP carrier protein T1 - mouse
N,Alternate names: adenine nucleotide carrier
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-195 #sequence_revision 06-Jan-19
C;Accession: S37210
R;Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 19
A;Reference number: S37210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-298 < LAP>
A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
C;Genetics:
C;Genetics:
A;Gene: ANC1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Superfamily: ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                       A; Molecule type: mRNA

A; Residues: 1-298 < PON*

A; Residues: 1-298 < PON*

A; Cross-references: GB: M24102; NID:g529414; PIDN:AAA30768.1;

R; Rasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A; Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two di

A; Reference number: A24822; MUID:86295775; PMID:3017341

A; Accession: A24822
                                                                                                                                                                                                                          C;Species: Bos primigenius taurus (cattle)
(;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; Ā03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 198
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
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    ;Molecule type: mRNA
;Residues: 208-298 <RAS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
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Pred. No. 7.6e
10; Mismatches
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A;Reference number:
A;Accession: A61343
A;Accession: A61343
A;Molecule type: protein
A;Residues: 205-298 <BAB>
R;Oettmeier, W.; Masson, K.; Kalinna, S.
R;Oettmeier, W.; Masson, C.; Kalinna, C.; Kalinna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: This protein is synthesized in the cytosol and transported into the mi C;Complex: homodimer C;Complex: homodimer C;Function:
A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATI A;Note: located in the inner mitochondrial membrane C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; F;5-99/Domain: ADP,ATP carrier protein repeat homology ACP1.
ADP,ATP carrier protein T2 - human

NJP,ATP carrier protein T2 - human

N;Alternate names: mitochondrial ADP,ATP translocase 2

C;Species: Homo sapiens (man)

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C;Accession: A29132; C28116

R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987

A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat A;Reference number: A29132; MUID:87166056; PMID:3031073

A;Accession: A29132
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R;Babel, W.; Wachter, B.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A;Title: Amino acid sequence determination of the ADP,ATP
A;Reference number: A61343; MUID:82046808; PMID:6271240
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F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status
F;52/Modified site: N6-methyllysine (Lys) #status predicted
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A; Residues: 2-51,'X', 53-70,'X', 72-109,'X', 111-298
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Comment: This protein is synth
Complex: homodimer
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Pred. No. 2.2e-124;
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PMID:7867632
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ADP,ATP carrier protein T3 - human
N;Alternate names: ADP,ATP carrier protein T2
C;Species: Homo sapiens (man)
A; Molecule type: mRNA
A; Residues: 36-104,'R',106,'A',109-298 <HOU>
A; Cross-references: GB: J03592; NID: g339722; l
A; Experimental source: liver
                                                                                                                R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116
                                                                                                                                                                                                                                                                                                                                A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03894
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: C28116
                                                                                                                                                                                                                                                                                                                                                                                                  R;Cozens, A.L.; Runswick, M.J.; Walker, J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-298 <BAT>
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
                                                                                                                                                                                                                                                            A; Molecule type:
A; Residues: 1-298
                                                                                                                                                                                                                                                                                                                  A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:ANT2; T3; 2F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man);Date: 17-Mar-2000 #text_change;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change;Accession: S03894; B28116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology; Reywords duplication; homodimer; mitochondrion; transmembrane protein 75-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
1110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
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                                                                                                                                                                                                                                                               1-298 <COZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQGIIIYRAAYFGVYDTAKGMLPDÞKNVHIFVSWMIAQSVTAVAGLLSYÞFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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Pred. No. 2.5e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (misidentification); mitochondrial
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PIDN: AAA36750.1;

PID:g339723

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C;Species: Bos primer: 1993 #sequence_revible....
C;Date: 03-Mar-1993 #sequence_revible....
C;Accession: B43646
R;Powell, S.J; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1999
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed difference number: A43646; MUID:89229093; PMID:2540808
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Residue: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <POW>
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology <ACP1-F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP1-F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Gene: GDB:ANT3; ANT3Y
A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp2.32-Xp22.32; Yp11.3-Yp11.3
A;Mote: there may be some confusion in the assignment of sequences for GDB:ANT2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein transmembrane protein
F;2-298/product: ADP,ATP carrier protein #status predicted <MAT>
F;5-299/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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B43646
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C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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                                                                                                                                                                                                                                                                                                   h 88.9%; Score 1380.5; DB 2
Similarity 86.9%; Pred. No. 2.5e-117;
59; Conservative 21; Mismatches 17;
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     GAAGATSLCFVYPLDFARTRLAADVGKSGSEREFRGLGDCLVKITKSDGIRGLYQGFNVS
                                 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                             MGDHAWSFLKDFLAGAVAAAVSKTAVAFIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                                                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                               I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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87.2%; Pred. No. 8.8e-118;
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A;Reference Humany
A;Accession: S31935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
C;Keywords: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                                                                                                                              ADP, ATP carrier protein - African malaria mosquito C; Species: Anopheles gambiae (African malaria mosquito) C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text C; Accession: S31935; S31936 C; Accession: S31935; S31936 R; Beard, C.B.; Crews-Oyen, A.B.; Colling, F.H. submitted to the EMBL Data Library, February 1993 A; Description: A cDNA encoding an ADP/ATP carrier from 1
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S31935
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; C;Superfamily: ADP,ATP carrier protein; C;Keywords: duplication; transmembrane protein
E;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
E;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
E;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S31814
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Pred. No. 3e-116;
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C;Species: Caenornabultis C-2. C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C;Accession: T25850 R;Gelsel, C: Stellyes, L. submitted to the EMBL Data Library, December 1996 submitted to the EMBL Data Library Data 
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A; Introns: 4/1; 191/2
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A;Status: preliminary; translated
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A; Reference number: Z20099
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                                                                                                                AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSGRKGA
                                                                                                                                                                                               LCFVYPLDFÄRTRLÄÄDVGKANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                                                                                                                                                                                   AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                 FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSGRK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIGAFCGGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLGSGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 1045.5; DB 2; 69.8%; Pred. No. 5.6e-87; Live 36; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1142.5; DB 1; Length; Pred. No. 8.8e-96; 26; Mismatches 42; Indels
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                                                                                                                   A; Map position: A; Introns: 20/1; C; Superfamily: A
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C; Accession: T25371
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T23207
                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T25371
                                                                                                                                                                                            A:Gene: CESP:T27E9.1
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                                                                                                                                                                                                                                                                                                A; Residues: 1-300 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  문
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                                                                                                                     ;Introns: 20/1; 41/3;;Superfamily: ADP,ATP
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Best Local
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hypothetical protein T27E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                     A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; A;Experimental source: clone T27E9
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                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library,
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A; Cross-references: EMBL: Z68218; PIDN: CAA92472.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALWRGNLANVIRYEPTQALNEAFKOTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                115/2 carrier protein;
                   66.8%; Score 1037.5; DB 2; 69.1%; Pred. No. 2.8e-86;
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  38;
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  Mismatches
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ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Ju
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C; Superfamily: /
F; 9-103/Domain:
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A;Residues: 1-300 <LET>
A;Cross-references: EMB
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A; Accession: T15206
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C;Species: Caenorhabditis elegans
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                                                                                                                                                       DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                        AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRWMMQSGRKGA
                                                                                                                                                                                                                                                                                              LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR
                                                                                                                                                                                                                                                                                                                                                                 FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGF
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                                                                                                                             DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDBIQHLI 300
                                                                                                                                                                                                  AAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRRMMQSGRK--
                                                                                                                                                                                                                                                                      LCFVYPLDFVRTRLGADVGKGVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                                                                                                                                                                                                                          AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                 FLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVLARVPKEQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDBIQKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMYQSGRKGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
#sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN
:e: strain Bristol N2; clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.7%; Score 1005.5; DB 2; 66.0%; Pred. No. 2.2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-301 <HAT>
A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
A;Cross-references: EMBL:X83551; NID:g622334; PIDN:CAA58541.1; PID:g623335
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                               NyAlternate names: ADP/ATP transporter
C;Species: Plasmodium falciparum
C;Date: 07-May-1995 #sequence revision 01-Sep-1995 #text_change 09-J-C;Accession: S68993; S51132
R;Hatin, I.; Jaureguiberry, G.
Bur. J. Biochem. 228, 86-91, 1995
ByT. J. Biochem. 228, 86-91, 1995
A;Title: Molecular characterisation of the ADP/ATP-transporter cDNA
A;Reference number: S68993; MUID:95188918; PMID:7883016
A;Accession: S68993
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R;Hilgarth, C; Sauer, N; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde A;Reference number: A41677; MUID:92084708; PMID:1748677
A;Accession: A41677
A;Status: preliminary
A;Status: preliminary
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A; Residues: 1-339 <HIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 QGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLAG
    65
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                                                                         SPIKDFIAGAVAAAVSKTAVAPIERVKILIQVQHASKQISA--EKQYKGIIDCVVRIPKE
QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG 124
                                                     KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVIRGMGGAFVLVLYDBIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
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58.3%;
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                                                                                                                                           Score 904.5; DB 2;
Pred. No. 3.1e-74;
A. Mismatches 70;
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                               EMBL; J04982; AAAS1736.1; -
EMBL; BC008664; AAH08664.1;
PIR; A44778; A44778.
                                                                                                                                                     PRINTS; PR00784; MTUNCOUPLING
                                                                                                                                                                  Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                           InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
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-!- FUNCTION: CATALYZES THE EXCHANGE OF
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Schnerch A., Schein J.E., Jones S.J.
                                                                                               TRANSMEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Level
                                                                                                                                                                                                                                                GO:0005887; C:integral to plasma membrane; TAS. GO:0005739; C:mitochondrion; TAS. GO:0015207; F:adenine transporter activity; TAS. GO:0006091; P:energy pathways; TAS. GO:0000002; P:mitochondrial genome maintenance; TAS.
                                                                                                                                                                                                                                     GO: 0006832; P: small molecule transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distinct genes for ADP/ATP translocase are expressed 1 in adult human liver.";
Natl. Acad. Sci. U.S.A. 85:377-381(1988).
                                                                                                                                      PS00215; MITOCH_CARRIER;
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                       Shinohara Y., Kamida M., Yamazaki N., Terada H.;
"Isolation and characterization of cDNA clones and a genomi encoding rat mitochondrial adenine nucleotide translocator. Biochim. Biophys. Acta 1152:192-196(1993).

-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
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                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley, and Wistar; TISSUE-Heart, and Liver; MEDLINE-94002161; PubMed-8399300;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                     EXTENT, IN BRAIN AND KIDNEY.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                  SUBUNIT: Homodimer
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98.3%;
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V=N (IN PEO).
/FTId=VAR_012112.
G->A (IN REF. 3).
KGA->RR (IN REF. 3).
V->L (IN REF. 3).
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                                                                                                                              MUSCLE
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license agreement (See http://www.isb-sib.

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homologs.";
Mamm. Genom
[2]
                                                                                                                   ADTI_MOUSE STANDARD; PRT; 298 AA. P48962; Q62164; O1-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) ADP_ATP carrier protein, heart/skeletal muscle translocase 1) (Adenine nucleotide translocator SIC25A4 OR ANTI OR ANCI.
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TRANSMEM
                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=97059403; PubMed=8903
                                                                                                                                                                                                   MOUSE
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REPEAT
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PROSITE;
                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      Ellison J.W.,
                                                                                 NCBI_TaxID=10090;
                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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EMBL; D12770; BAA02237.1;
PIR; I60173; I60173.
                            "Rapid evolution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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Local
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          Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an email to
                                                                                                                                                                                                                                       QSGRKGADIMYTGTVDCWRKIAKDEGRKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLFDPKNVHIFVSMMIAQSVTAVAGLLSYPFDTVRRRMM
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                           X., Franc
                                                                                                                                                                                                                                                                                                                CFVYPLDFARTRLAADVGKGSSQRBFNGLGDCLTK1FKSDGLKGLYQGFSVS
                                     PubMed=8903724;
K., Francke U.,
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                                                                                             Chordata;
Rodentia;
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                            pseudoautosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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Pred. No. 4.7e-124;
9; Mismatches 7;
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                                                                                           Craniata; Vertebrata; | Sciurognathi; Muridae;
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(POTENTIAL).
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                                     Shapiro L.J.;
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Murinae; Mus
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Blaards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Myeng A.C., Shevchenko Y., Bouffard G.G.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmu
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EMBL; X74510; CAA52616.1; -.
EMBL; AP240002; AAF64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC026925; AAH26925.1; -.
PIR; S37210; S37210.
MGD; MGI:1353495; S1c25a4.
InterPro; IPR002007; Mit_uncoupling.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR002031; Mitoch carrier.
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Multigene famil
TRANSMEM 12
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STRAIN-BALB/c; TISSUE-Muscle;
STRAIN-BALB/c; Costet P.;
STRAIN-BALB/c; TISSUE-Muscle;
STRAIN-BALB/c; TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
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RESULT 4
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ADT1 B
ADT1 B
AC P02752
DT 21-UUL
DT 16-OCT
DB ADP, TO
COC EURAPY
OC E
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Best Local Similarity
Matches 280; Conser
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REPEAT
CONFLICT
SEQUENCE
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P02722;
                                                                                                                                        an unusually short 3'-noncoding sequence.";
Biochem. Biophys. Res. Commun. 138:850-857
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADI
                                                                                                                                                                                                         MEDLINE=86295775; PubMed=3017341;
Rasmussen U.B., Wohlrab H.;
"Bovine cardiac mitochondrial ADP/ATP-carrier: two
                                                                                                                                                                                                                                                                                                                                              "Complete amino mitochondria.";
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-82188267; PubMed-7076130;
Aquila H., Misra D., Eulitz M., Klingenberg M.;
"Complete amino acid sequence of the ADP/ATP carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 28:866-873 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89229093; PubMed=2540808;
Powell S.J., Medd S.M., Runswick M.J.,
"Two bovine genes for mitochondrial AD
differences in various tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLC25A4 OR ANT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase (Adenine nucleotide translocator 1) (ANT 1).
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                                                                                                                                                                                                                                                                               SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier family
                                                                          SUBCELLULAR LOCATION:
                                                                                                 SUBUNIT: Homodimer
                                                                                                                   MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSGRKGADIMYTGTVDCWRKIAKDEGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKYV
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                                                                                                                                                                                                                                                                               FROM N.A.
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Pred. No. 8.7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcochondrion;
Multigene famil
INIT MET 1
INIT MET 1
MOD RES 1
TRANSMEM 11
TRANSMEM 11
TRANSMEM 116
TRANSMEM 116
TRANSMEM 175
TRANSMEM 175
TRANSMEM 175
TRANSMEM 213
TRANSMEM 272
                               DDT2 MOUSE STANDARD; PRT; 298 AA.
P51881; Q61311;
01-QCT-1996 (Rel. 34, Created)
01-QCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (
Adenine nucleotide translocator 2) (ANT 2).
SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
REPEAT
SEQUENCE
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR002030; Mit_unco
InterPro; IPR001993; Mitoch_c
InterPro; IPR001993; Mitoch_c
Pfam; PF00153; Mito_carr; 3
PRINTS; PR00926; MITOCARRIER.
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EMBL; M24102; AAA30768.1; -.
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PS00215; MITOCH CARRIER; 3.

ndrion; Inner membrane; Repeat;

ne family; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                              GRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                   AGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSVQ
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Pred. No. 6.8
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METHYLATION
Craniata; Vertebrata; i
Sciurognathi; Muridae;
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3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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   Buteleostomi;
; Murinae; Mus
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NCBI_TaxID=10090;

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SALALAR BERREAR BER
Query Match
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EMBL; U10404; AAA19009.1; -.
EMBL; X70847; CAA55196.1; -.
EMBL; AF240003; AAF64471.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laplace C. Submitted
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20432087; PubM
Levy S.E., Chen Y.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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TISSUE=Skeletal muscle;
Sheldon J.G.;
Thesis (1995), University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97059403; PubMed=8903724;
Ellison J.W., Li X., Francke U., Shapiro L.J.;
"Rapid evolution of human pseudoautosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ER European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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Similarity
                                                                                                                                                                                                                                                                                PR00784; MTUNCOUPLING.
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73
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117
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273
                                                                                                                                                                                                                                                                 PS00215; MITOCH CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and this statement is not removed.
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                                   Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCARRIER. PRINTS; PR00784; MTUNCOUPLING.
                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterization of cDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator.", Biochim. Biophys. Acta 1152:192-196 (193).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP, ATP carrier protein, fibroblast isoform (
Adenine nucleotide translocator 2) (ANT 2).
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Q09073;
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                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. U
              PROSITE; PS00215; MITOCH CARRIER; 3
Mitochondrion; Inner membrane; Repe
                                                                                                       EMBL; D12771; BAA02238.1;
InterPro; IPR002067; Mit_c
                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley; TISSUE=Liver; MEDLINE=94002161; PubMed=8399300; Shinohara Y., Kamida M., Yamazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                            InterPro; IPR002030; Mit_unc
InterPro; IPR001993; Mitoch
                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                 inner membrane.
TISSUB SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                         DOMAIN:
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                                                                ; Mit_carrier.

; Mit_uncoupling.

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            membrane;
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Sciurognathi; Muridae; Murinae; Rattus.
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            Repeat;
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              Transmembrane;
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Matches 266
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13-AUG-1987 (Rel. 05, 0
01-OCT-1994 (Rel. 30, I
28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                                                                                                          28-PEB-2003 (Rel. 41, Last amoutation update)
ADP, ATP carrier protein, fibroblast isoform (Adenine nucleotide translocator 2) (ANT 2).
SLC25A5 OR ANT2.
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MEDLINE-90375457; PubMed=2168878;
MEDLINE-90375457; PubMed=2168878;
MEDLINE-90375457; PubMed=2168878;
MEDLINE-POSTATE

KERNEY

The human fibroblast adenine nucleotide cloning and sequence.";
Cloning and sequence.";
J. Biol. Chem. 265:16060-16063(1990).
                                                                      growth-regulated
J. Biol
                  SEQUENCE FROM N.A.
Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
Mazzarella R.A., Schlessinger D., Chen E.Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                   "Molecular cloning
                                                                                                                 Battini
                                                                                                                        SEQUENCE FROM N.A. MEDLINE=87166056; PubMed=3031073;
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Mammalia; Eutheria;
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Pred. No. 9e-
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the Swiss Institute of Bioinformatics and the bactween the Swiss Institute Institute. There are no rest
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PRINTS; PR00784; MTUNCOUPLING.
PRO07215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0015207; F:ademine transporter activity; TAS. GO; GO:0006832; P:small molecule transport; TAS. InterPro; IPR002067; Mit_carrier. InterPro; IPR002030; Mit_uncoupling. InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           SEQUENCE
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EMBL; J02683; AAA35579.1; -.
EMBL; L78810; AAB39266.1; -.
EMBL; AC004000; AAB96347.1; -.
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c. Natl. Acad. Sci. U.S.A. 85:377-381(1988)
FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
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Pred. No. 5.8e-118;
7; Mismatches 15;
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G -> E (IN REF. 2).
R -> L (IN REF. 4 AN
V -> G (IN REF. 5).
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RMDLINE-22388.57; pubMed=12477932;

RMDLINE-22388.57; pubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max R., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Joain F., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Schmutz J., Myers R.M.,

Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.",

Parce. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Margolin J.F.;
Submitted (JUL-2000)
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MEDLINE=89236396; PubMed=2541251;
Cozens A.L., Runswick M.J., Walker J.E.;
"DNA sequences of two expressed nuclear genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa;
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Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase ar
level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988)
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                             MEDLINE=88124845;
                                                                                                                                                                                                           SEQUENCE OF 3
TISSUB=Liver;
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, Yu W., Tang
n J.F.;
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                                                                                                                                                                             PubMed=2829183;
                                                                                                                                                                                                                                FROM N.A
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mei G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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EMBL; BC014775;
PIR; S03894; S03
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InterPro; IPR011993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005744; C:mitochondrial inner membrane translocase GO; GO:0005471; F:ATP/ADP antiporter activity; NAS. GO; GO:0006854; P:ATP/ADP exchange; TAS. InterPro; IPR002067; Mit carrier. InterPro; IPR002030; Mit_uncoupling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Supersend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00215; MITOCH
Mitochondrion; Inner memb
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1; AY007135; AAG01998.1; -.
1; BC007295; AAH07295.1; -.
1; BC007850; AAH07850.1; -.
1; BC008737; AAH08737.1; -.
1; BC008935; AAH08935.1; -.
1; BC014775; AAH14775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inner membrane.
DOMAIN: COMPOSED OF
SIMILARITY: Belongs
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SUBCELLULAR LOCATION:
                                             181
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                                                                                                                                                                                                 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                OSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
                                                                                           GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                          I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                   IPKEQGELSFWRGNLANVIRYEPTQALNEAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                     MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
QSGRKGADIMYTGTVDCWRK1FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
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298
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87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARRIER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the mitochondrial carrier family.
                                                                                                                                                                                                                                                Score 1385.5;
Pred. No. 8.4e
                                                                                                                                                                                                                                                                               KHTQ -> RHA (IN REF. 4).
S -> F (IN REF. 3; AAH14775)
; 18534E9F0E49672F CRC64;
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics and the
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                8.4e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no
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                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89229093; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial AD! differences in various tissues."; Biochemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP, ATP carrier protein, isoform T2 nucleotide translocator 3) (ANT 3). SLC25A6 OR ANT3.
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupli
InterPro; IPR001993; Mitoch carri
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M24103; AAA30769.1; -. PIR; B43646; B43646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, isoform T2 (ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P32007;
01-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00926; MITOCARRIER
                                                                                 MGDHAWSFLKDFLAGAVAAAVSKTAVAFIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
I PKEQGVLS FWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                          I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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och_carrier.
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                                                                                                                                                                         21;
                                                                                                                                                                                           Score 1380.5;
Pred. No. 2.46
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Transmembrane; Transport;
                                                                                                                                                                           Mismatches
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P/ATP translocase expressed
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RESULT 10
                 PRESENTATION OF THE PROPERTY O
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RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.B., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter B.G., Helt G., Wilson C.R., Miklos G.L.G.,
RA Bartl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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"A CDNA clone encoding the ADF/AL

melanogaster shows a high degree

anp/ATP translocases.";

ac. 44-50(1992).
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT DROME STANDARD; PRT; 299 AA. Q26365; P91614; Q262367 (29530; Q9VZ70; Q267011-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocate) (Advisor) (ATP) (Stress sensitive B protein).
SESB OR A/A-T OR CG15944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila."; Experientia 50:749-762(1994).
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Zhang Y.Q., Davi
Submitted (JAN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Davis A.W., (JAN-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the ADP/ATP translocase igh degree of similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Ashburner
databases.
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Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian
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ARA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Melson D.R., Remington K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Palazzolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RI Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL; $43651; AAB23114.1; -.

EMBL; $71762; AAB31734.3; -.

EMBL; $710618; CAA71628.1; -.

EMBL; AB003484; AAF47957.1; -.

EMBL; AX070894; AAL28526.1; -.

EMBL; AX070894; Cimitochondrial inner membrane; IE; GO; GO:0006743; Cimitochondrial transport; IMP. InterPro; IPR002067; Mit carrier.

InterPro; IPR001993; Mitoch_carrier.

Pfam; PF00153; mito_carr; 2.

PRINTS; PR00153; mito_carr; 3.

PROSITE; PR002215; MITOCH_CARRIER; 3.
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Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley; TISSUE=Larva, Ova
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Catalyzes the exchange of ADP mitochondrial inner membrane. SUBUNIT: Homodimer (By similarity). SUBCELLULAR LOCATION: Integral membrane
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232
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Kronmiller B.,
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          2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
GI -> QV (IN REF. 1 AND 2).
I -> Y (IN REF. 1).
MISSING (IN REF. 1 AND 2).
G -> A (IN REF. 1).
TG -> P (IN REF. 1 AND 2).
A -> G (IN REF. 1).
                                                                                                                                                                                               Repeat; Trans (POTENTIAL).
2 (POTENTIAL).
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D51F3E2A70BD59E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P., Yu C., Ch.,
Pacleb J.M.,
                                                                                                                                                                                                                                    Transmembrane;
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DP and ATP
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14 75 119

31 93 136

Repeat; Transmembrane; (POTENTIAL). (POTENTIAL). (POTENTIAL).

Transport.

Mitochondrion; Inner

membrane;

PROSITE;

F00153; mito_carr; 3.
PR00926; MITOCARRIER.
; PS00215; MITOCH_CARRIER; 3.

_carrier.

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AREST CONTROL TO THE SECOND DESCRIPTION OF T
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Matches 232
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Q27238;
01-NOV-1997
01-NOV-1997
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01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
ADP,ATP carrier protein (ADP/ATP trans
translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translocator) (ANT).
Anopheles gambiae (African malaria mosquito).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta,
Neoptera, Endopterygota, Diptera, Nematocera, Culic
NCBI_TaxID=7165,
                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                           the Buropean Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94348635; PubMed=8069414;
Beard C.B., Crews-Oyen A.E., Kumar V.K.,
"A CDNA encoding an ADF/ATP carrier from
                                                                                                                                   InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carri
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                           EMBL; L11618; AAB04104.1; EMBL; L11617; AAB04105.1;
                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. between the Swiss Institute of Bio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the mitochondrial carrier family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inner membrane.
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Pred. No. 7.3e
26; Mismatches
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Culicoidea; Anopheles.
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Best Local Sim
Matches 223;
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01-JUL-1993 (Rel. 26, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
                                                                                                                                                                                                                                                             Hilgarth C., Sauer N., Tanner W.; "Glucose increases the expression of the glyceraldehyde-3-phosphate dehydrogenase J. Biol. Chem. 266:24044-24047(1991).
-i- FUNCTION: CATALYZES THE EXCHANGE OF A MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                               translocator) (ANT).
Chlorella kessleri.
              Pfam; PF00153; mito_carr; PRINTS; PR00926; MITOCARRI
                                                             EMBL; M76669; AAA330;
PIR; A41677; A41677.
                                                                                                  use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last annotation update) ADP, ATP carrier protein (ADP/ATP translocase)
                                    InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                          MEDLINE=92084708; PubMed=1748677;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3074;
                                                                                                                                                                                                                                       SUBUNIT: Homodimer (By similarity) SUBCELLULAR LOCATION: Integral mem
                                                                                                                                                  European
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MITOCH_CARRIER; 3.
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RESULT 13
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion; 1
TRANSMEM 45
TRANSMEM 108
TRANSMEM 151
TRANSMEM 209
TRANSMEM 248
TRANSMEM 304
SEQUENCE 339;
                                   This SWISS-PROT entry is copyright. It is produced through a cobweven the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
                                                                                                                                                                                                               Sharpe J.A., Day A.;

"Structure, evolution and expression

translocator gene from Chlamydomonas

Mol. Gen. Genet. 237:134-144 (1993).

-I- FUNCTION: CATALYZES THE EXCHANGE
                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat
ADP, ATP carrier protein (ADP/ATP translocas
translocator) (ANT).
                                                                                                                                                                         ++
                                                                                                                                                                                                                                                                                                STRAIN=FUD44-R2
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                     Chlamydomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P27080;
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT_CHLRE
EMBL; X65194; CAA46311.1;
                                                                                                                                                 -
                                                                                                                                                                                                                                                                                 MEDLINE=93204887;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                         MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                DOMAIN:
                                                                                                                                   SIMILARITY: Belongs to
                                                                                                                                                              inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYRGAYFGLYDTAKGVLFKDERTANFFAKWAVAQAVTAGAGVLSYPFDTVRRRLMWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYRAAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATSLCFVYPLDFARTRIAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEK--QYKGIIDCVVRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>AGSLLIVÝ PLDFARTRLAADVGSGKSREFTGLVDCLSKVVKRGGPMALÝ QGFGVSVQGII</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKFI
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108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                   PubMed=8455552;
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168
228
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                                                                                                                                                                                                                                                                                                                                                       Chlamydomonas
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                                                                                                                                   THREE HOMOLOGOUS DOMAINS. to the mitochondrial carrier family.
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Pred. No. 7.6e-80;
0; Mismatches 65
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
54779734A33B3942 CRC64;
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                                                                                                                                                                                                                                           of the mitochondrial ADP/ATP reinhardtii.";
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RESULT 14
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AC P047
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Best Local
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TRANSMEM 12
TRANSMEM 74
TRANSMEM 116
                                                                              SEQUENCE (
                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
01-AUG-1992 (Rel. 23, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
ADP,ATP carrier protein 1, mitochon
translocase 1) (Adenine nucleotide
ANT1 OR ANT-G1.
STRAIN=CV. B3/N;
MEDLINE=89338399; PubMed=2547608;
Leaver C.J., Bathgate B., Baker A.;
Leaver C.J., Bathgate B. adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT1 MA
P04709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM TRANSMEM
                                                                                                                                                                                                                      STRAIN=MUTIND-FR7205034;
MEDLINE=91322533; PubMed
                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                        ranslocator from Plant Mol. Biol.
                                                                                                                                                                            MEDLINE-91322533; PubMed-1863785; Winning B.M., Day C.D., Sarah C.J. "Nucleotide sequence of two cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                      mays (Maize)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245
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                                                                                                                                                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ
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                                                                                                    59-387
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116
178
217
273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S30259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                        n Zea mays L.";
17:305-307(1991)
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133
197
234
291
                                                                                                    FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                            annotation update)
mitochondrial precursor
cleotide translocator 1)
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Pred. No. 1e-6
19; Mismatches
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(POTENTIAL).
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SEQUENCE
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between
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-- FUNCTION: CATALYZES THE EXCHANGE OF ADP MITOCHONDRIAL INNER MEMBRANE.
-- SUBUNIT: Homodimer.
-- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X57556; CAA40781.1; -.
EMBL; X15711; CAA33742.1; -.
EMBL; X02842; CAA26600.1; -.
PIR; S14876; S14876.
MaizeDB; 17145; -.
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InterPro; IPR001993; Mitoch carri
Pfam; PF00153; Mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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    -!- SIMILARITY: Belongs to the mitochondrial carrier family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85297781;
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Bur. J. Biochem.
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                                                                                                                                               IIIYRAAYFGVYDTAK-----GMLFDFKNVHIFVSWMIAQSVTAVAGLLSYFFDTVRRRM
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MMTSGEA---
                                                                                                                IIVYRGLYFGLYDSIKPVVLTGNLQD----NFFASFALGWLITNGAGLASYPIDTVRRRM
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Pred. No. 2.4e-60;
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-> Y (IN REF. 3).
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A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G. V., Ussery D., Barrell B.G., Nurse P.;
RI Nature 415:871-880(2002)
CC MITTOCHONITAL INNER MEMBRANE
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ANCI OR SPBC530.10C.
Schizosaccharomura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q09T88;
01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, I
28-FEB-2003 (Rel. 41, I
                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
  modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.; "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
NCBI_TaxID=4896;
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                                                                                                                                                                                       MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                          DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
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  non-profit institutions as long and this statement is not removed.
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                    GATSLCFVYPLDFARTRLAAD---VGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV
                                                                                                                                                 EOGELGEWRGNLANVIRYEPTOALNEAFKDKYKOLFLGGVDRHKOEWRYEAGNLASGGAA 123
                      QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
                                             VGIVVYRGLYFGMYDTLKPVVLVGPLEGNFLASFLLGWAVTTGSGVASYPLDTIRRMMM
                                                             QGIIIYRAAYFGVYDTAKG-MLEDEKNVHIFVSWMIAQSVTAVAGLLSYEEDTVRRRWMM
                                                                                       GAASLLFVYSLDYARTRLANDAKSAKKGGERQFNGLVDVYRKTYRSDGLRGLYRGFGPSV
                                                                                                                                   BEGVISLWRGNTANVLRYFPTQALNFAFKDKFKKMF-GYKKERDGYAKWFAGNLASGGAA
                                                                                                                                                                                                                                                                                                                                                            PS00215; MITOCH_CARRIER; 2.
 TSGEA---VKYSSSFECGROILAKEGARSFFKGAGANILRGVAGAGVLSIYDQVQ 314
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93
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Pred. No. 4.4
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1 (POTENTIAL).
2 (POTENTIAL).
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Search completed: December 18, 2003, 12:41:23 Job time : 9.31467 secs

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Listing first 45 summaries
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1 MGDHAWSFLKDFLAGAVAAA.....LRGMGGAFVLVLYDEIKKYV 297
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60 	Query Match 94.3%; Score 1464.5; DB 6; Length 298; Best Local Similarity 94.6%; Pred. No. 7.2e-129; Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;	SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;	Membrane; Transmembrane; Transport.	PRINTS; PRO0784; MITUNCOUPLING.	PRINTS; PR00926; MITOCARRIER.	0		InterPro; IPR002067; Mit carrier.	1993; Mitoch	L: AB009386: BAA23777.1:	-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.	skeletal muscle.";		ğ	Yamaguchi N., Kasai M.;	TISSUE=Skeletal muscle;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9986;	Lagomorpha; Leporidae; Oryctola		Oryctolagus cuniculus (Rabbit).		(TrEMBLrel. 23, Last annotation	(TrEMBLrel. 06,	01-JUN-1998 (TrEMBLrel. 06, Created)		O46373 PRELIMINARY; PRT; 298 AA.	ULT 1 373

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01-JUN-2002
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL, AK078077; BAC37117.1; -.
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STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=22354683; PubMed=12466851;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Query Match
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Matches 263; Conserv
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Shinohara Y., Tanida K., Terada H.;
Yamazaki N., Shinohara Y., Tanida K., Terada H.;
"Structural properties of mammalian mitochondrial ADP/ATP carriers:
identification of possible amino acids that determine functional
differences in its isoforms.";
Mitochondrion 1:371-379(2002).
EMBL; AB065433; BAB4673.1; --
EMBL; AB065433; BAB4673.1; --
                                                                                                                                                         SEQUENCE FROM N.A.

Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba "Cold-induced mitochondrial uncoupling and expression and ANT mRNA in chicken skeletal muscle.";

FRBS Lett. 0:0-0(2002).

EMBL; ABOBS666; BAC15533.1; -.

SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PROSITE; PS00215; MITOCH CARRIER; 3.
SEQUENCE 298 AA; 32955 MM; CB689
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP/ADP antiporter.
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        Conservative
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    89.7%; Score 1392.5; DB 13
88.3%; Pred. No. 4e-122;
tive 18; Mismatches 16;
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23,
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Pred. No. 6.6e-124;
L6; Mismatches 13;
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MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR

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Miura I, Ohtani H, Makamura M, Ichikawa Y., Saitoh K.;

"The origin and differentiation of the heteromorphic sex chro
I Z, W, X, and Y in the frog Rana rugosa, inferred from the sec
I a sex-linked gene, ADP/ATP translocase.";

L Mol. Biol. Evol. 15:1612-1619(1998).

- !- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL; AB008457; BAJA5507.1; -.

R InterPro; IPR002030; Mitoch_carrier.

R InterPro; IPR002030; Mit_uncoupling.

R InterPro; IPR002030; Mit_uncoupling.

R Pfam; PP00153; mito carr; 3.

R PRINTS; PR00784; MITOCH CARRIER.

PRINTS; PR00784; MITOCH CARRIER; 3.

R PROSITE; PS00215; MITOCH CARRIER; 3.

Membrane; Transmembrane; Transport.

SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
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Best Local !
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Q9YIC4;
01-MAY-1999
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana rugosa (Wrinkled frog).
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                                                                     GAAGATSLCFVYPLDFARTRLAADVGKAGADREFKGLGDCLAKIFRSDGLKGLYQGFNVS
                                                                                                                                  I PKEQGFLSFWRGNLANV I RYFPTQALMFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTAVAGFASYPFDTVRRRMM
                                       VQGIIIYRAAYFGVYDTAKGM1FDPKNVHIFVSWMIAQSVTAVAGL1SYPFDTVRRRWMM 239
                                                                                                                     MTDAAISFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIMDCVVR
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                                                                                                                                                                                                                  88.7%; Score 1377.5; DE
86.6%; Pred. No. 1e-120;
Live 23; Mismatches 1
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Ranidae; Rana
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                                                                                                                                                                                                                                            298;
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                                                                                                                                                                                                                   Gaps
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RESULT 7
Q8JHIO
Q8JHIO
Q8JH
AC Q8JH
DT 01-C
DT 01-N
DB Solv
GN SLC2
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Best Local (
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 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Solute carrier family 25 member 5 protein.
SLC25A5.
                                                                     Q8JHI0
                                                            Q8JHI0;
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중 유 8 밁 8 망 ð 밁 ঠ

PRELIMINARY;

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EMBL; AB008463; BAA36513.1; ---
EMBL; AB008465; BAA36506.1; --
EMBL; AB008461; BAA36506.1; --
EMBL; AB008461; BAA36512.1; --
EMBL; AB008462; BAA36512.1; --
EMBL; AB008462; BAA36512.1; --
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR007926; MITOCARRIER.
PRINTS; PR007926; MITOCARRIER.
PRINTS; PR007184; MTUNCOUPLING.
PROSITE; PS00215, MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33054 MW; B0E23AD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=99083429; PubMed=9866197;

MIUTA I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh

MIUTA I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh

"The origin and differentiation of the heteromorphic s

"The visual and Y in the frog Rana rugosa, inferred from

a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP/ATP translocase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLÞDÞKNVHIFVSMMIAQSVTAVAGLLSYÞFDTVRRRMM 239
                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGRR-AQRBFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                         I PKEQGFVSFWRGNLANVIRYFPTQALNFAFKDKYKKI FLDNVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                  IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                     MTDAAISFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIMDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                            MGDHAMSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                         VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQTVTAVAGFASYPFDTVRRRMM
OSGRKGABIMYSGTIDCWKKIARDEGSRAFFKGAWSNVLRGMGGAFVLVLYDELKKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1377.5; DE
Pred. No. 1e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B0E23AD56F548D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 8

Q9PR12

ID Q9PR
AC Q9PR
AC Q9PR
AC Q9PR
DT 01-W
DT 0
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Best Local
    EMBL; AB008458; 1
EMBL; AB008458; 1
EMBL; AB008459; 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                     InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_nucoupling.
InterPro; IPR002030; Mitouncoupling.
IPR00153; mito_carr; 3.
IPR00153; mito_carrier.
IPRINTS; PR00926; MITOCARRIER.
IPRINTS; PR007184; MITOCH_CARRIER; 3.
IPR091TE; PR007185; MITOCH_CARRIER; PR091TE;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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EMBL; AF506216; AAM34660.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
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Golling G., Amster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
    BAA36510.1; -. BAA36508.1; -. BAA36509.1; -.
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rdam A., Sun Z., Antonelli M.,
M., Artzt K., Farrington S., )
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Last annotation update)
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Pred. No. 1.6e
22; Mismatches
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                                                                                                                                                                                                                                                                                                                                          Ichikawa Y., Saitoh K.;
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, Lin S.-Y.,
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"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Speci
T Dynamic Patterns of Expression During Development.";
Submitted (FEB-2000) to the EMBL/GenBank/DDB databases.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
EMBL; AF231347; AAF63471.1; --
R InterPro; IPR001993; Mitoch carrier.
R InterPro; IPR002067; Mit_carrier.
R InterPro; IPR002067; Mit_carrier.
R InterPro; IPR002067; Mit_carrier.
R InterPro; IPR002030; Mit_cuncoupling.
R FARNTS; PR00926; MITOCARRIER.
R PRINTS; PR00926; MITOCARRIER.
R PRINTS; PR00926; MITOCARRIER.
R PRINTS; PR00926; MITOCARRIER.
R PRINTS; PS00215; MITOCARRIER; 3.
Membrane; Transmembrane; Transport.

M Membrane; Transmembrane; Transport.
                  Matches
                                          Query Match
Best Local
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Best Local :
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01-MAR-2003
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR007184; MITOCARRIER.
PROSITE; PR007184; MITOCH_CARRIER; 3.
PROSITE; PR007215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
f M.
c Local 5.
257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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-2000 (TrEMBLrel. 15, L
-2003 (TrEMBLrel. 23, L
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                  Score 1366.5; DB 1:
Pred. No. 1.1e-119;
3; Mismatches 17;
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Pred. No. 1.9e-120;
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RESULT 11
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ID Q9NHW5
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Q95VA
ID VX
ID VX
ID VX
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Best Local S
Matches 236
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCHRARIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCE
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Q95VX4;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the
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                                                                                                                                                                                                                                                                                                     ATSLCFVYPLXFARTRLAADIGKGLEQREFTGLGNCIAKIFKSDGLVGLYRGFGVSVQGI
                                                                                                                                                                                                                                                                                                                           ATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI
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                                                                                                                 KKADILYKNTIDCWGKIYKTEGGAAFFKGAFSNILRGTGGAFVLVLYDEIKALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.2%; Score 1245.5; DB 5;
80.3%; Pred. No. 2.3e-108;
Live 25; Mismatches 32;
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P SRQUENCE FROM N.A.

P SRQUENCE FROM N.A.

CSTRAIN=SS mal seeking;

RT Chen Z., Fair J.A., Batterham P.;

RT CANA clone encoding the ADP/ATP translocase of Lucilia cuprina.";

RI Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AP218587; AAF32322.1; --

DR InterPro; IPR002067; Mitoch carrier.

DR InterPro; IPR002067; Mitoch carrier.

PFAnn; PF00153; mito_carr; 3.

DR PFANTS; PR00926; MITOCARRIER; 3.

PRINTS; PS00215; MITOCARRIER; 3.

Wembrane; Transpendrame; Transport.

CROHENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
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Best Local !
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20196006; PubMed=10731132;

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R., Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003
01-MAR-2003
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01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bephydra; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8IRA0
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Lucilla cuprina (Greenbottle fly)
Eukaryota, Metazoa, Arthropoda; H
Neoptera; Endopterygota; Diptera;
Calliphoridae; Lucilia.
                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                       CG16944-PC
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78.7%;
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Doyle

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RA Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

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RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

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RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P.,

RA Glodek A., Goong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Harris M.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Melson D.R., Nelson K.A., Nixon K., Suughsti M.P., Sanith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sanith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sanith T.,

RA Shue B.C., Stan M., Janis G., Jano Q., Zheng L.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhan
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A Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Bearson J., An H., Baldwin D., Amanatides P.G., Brandon K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,

Perriera S., Fries E., Galle R.F., Garg N.S., Decorge R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

"Sequencing of Drosophila melanogaster genome.",
                                                                                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman G., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003484; AAN09267.1; -. SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
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e EMBL/GenBank/DDBJ
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letz S.M.,
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01-NOV-1996
01-MAY-1999
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Submitted (APR-1999) to ti
-!- SIMILARITY: BELONGS TV
EMBL; U44832; AAA97882.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane, Transmembrane, Transport.
SEQUENCE 317 AA; 35005 MM; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cai Q., Greenway S.C., Storey K.B.; "Differential regulation of the mitochondrial ADP/ATP translocase in wood frogs under freezing stress."; Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana sylvatica (Wood frog).
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           121 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                     79.5%;
85.7%;
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Pred. No. 2.7e-107;
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Ranidae; Rana
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179 120 120

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Query Match

SEQUENCE FROM N.A

SEQUENCE FROM N.A. Adams M.D., Celniker

(MAR-2000)

to:

SEQUENCE FROM N.A.

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ID 04409
AC 04409
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  044093;
044093;
01-JUN-1998
01-JUN-1998
01-MAR-2003
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SEQUENCE
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InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit carrier.
Pfam; PP00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
MON TER 288 288
288
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Genetica 0.0-0(1997)
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER
EMBL; AF025799; AAB87884.1; --
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;

Bobytera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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AAY71032 standard; Protein; 298 B

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT2.

ARESULT ARESULT IN ARE Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MFT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

WO200026370-A2

11-MAY-2000

03-NOV-1998; 08-SEP-1999; 03-NOV-1999; 98US-0185904. 99US-0393441. 99WO-US25883.

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RESULT 2
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mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                               Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
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llarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                 entry)
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Pred. No. 2.3e-154;
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The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability CC transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact CC with other mitochondrial core components e.g. cyclophilins to cregulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a CC expression construct comprising a promoter operably linked to a CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein CC (e.g. green fluorescent protein (GPP) or a FTASH sequence). The novel expression construct can alter mitochondrial membrane permeability CC transition and/or alter the interaction between mitochondrial core CC components. The methods are useful for screening for agents that alter CC components. The methods are useful for screening for the prevention or treatment of diseases associated with altered mitochondrial function or CC treatment of diseases associated with altered mitochondrial function or CC distinctional cell survival, such as Alabaimer's disease, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 186pp; English.
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Velicelebi G,
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                                                                                                                                                                                                                                                                                           GAAGATSLCEVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                     OSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTDAALSFAKDFLAGGVAAAISKTAVAFIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                  IPKEQEVLSFWRGNLANVIRYPPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                                                              VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                                                                                                                                                                             GAAGATSI
VQGIIIXRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                             I PKEQEVLS FWRGNLANVIRY FPTQALNFAFKDKYKQI FLGGVDKRTQFWRY FAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AA;
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}, Davis RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 2.3e-154;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 298;
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                                                                                                                                                                                                                                                                             The invention relates to a recombinant expression construct (I) Comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant CC antipolypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide is culturing the host cell. (I) is also useful for targeting a polypeptide of interest. CC expressed as a fusion protein with the polypeptide of interest. CC expressed as a fusion protein with the polypeptide of interest. CC expressed as a fusion agent that binds to an ANT polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide, correlated by ANT1, ANT2 or ANT3 in a biological sample and for isolating CC aNT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide.
                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson C
Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 44; Fig 2; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10379;
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DB; AAS16689.
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                                                                        IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                     MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                    MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moos WH, Pei
                                                                                                                                                                                                                                                                    identifying an agent that interacts with an ANT polypeptide. sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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Y, Carroll AK;
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Pred. No. 2.3
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                                                                                                                                                                                          DB 23;
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12-JAN-2001;
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12-JAN-2001;
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12-JAN-2001;
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12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                            targets for treating diabet contacting an assay system modifiers with a test agent
                                                                                                                                                                                                                                                                                                  Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO18516 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seidel-Dugan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human insulin receptor signaling modifier SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2002
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DB; AAL48635.
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diabetes; metabolic syndrome;
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2001US-261461P.
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2001US-261513P.
2001US-261531P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate

Disclosure;

Page 160-161; 232pp; English.

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ISM F

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M function and for other applications related to the involvement of ISM INR signaling, and for identifying subjects having a predisposition to the diseases associated with INR signaling. The present sequence is an M protein described in the exemplification of the invention.

ISM function

Query Match

Similarity

99.4%;

Length

298

B

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ID 7AAX7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MT7; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidabettic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                   Anderson
Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
Recombinant construct encoding adenine nucleotide translocator
                                                            WPI; 2000-365619/31.
N-PSDB; AAD00521.
                                                                                                                                                                                                                                                                                              03-NOV-1998;
08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
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99US-0393441
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                                                                                                                                                                              Clevenger
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Pred. No. 2.6e
1; Mismatches
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                                                                                                                                                                              Wiley
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2.6e-153;
les 1;
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                                                                                                                                                                                    Miller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses a method to produce adenine nucleotide translocator (C (ANT) proteins or ANT is a nuclear encoded protein and a major component of constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine (C di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents (C or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for (C etect or isolate ANT in a biological sample, and therapeutically for (C with altered mitochondrial function, including Alzheimer's, Parkinson's (C and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, (C encephalopathy, lactic acidosis and stroyke (MELAS), hyperproliferative (C disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic cepllepsy red ragged fibre syndrome. The present sequence is an an acceptance of the process of the syndrome of the process of the syndrome of the process of the process of the syndrome of the process of
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAMSNVLRGMGGAFVLVLYDBIKK 296
                                                                                                                                                      VQGIIIYRAAYFGIYDTAKGMLDDFKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
|||||||||||||
                                                                                                                                                                                                                                    GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                   I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1454; DB 21;
Pred. No. 1.4e-144;
3; Mismatches 9;
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RRESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide
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25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                    in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system disease, such as localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, hemotactic/chemokinetic activity, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic, unosuppressant and cytostatic activity. The polynucleotides are useful
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)B; AAI58797.
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Zhou
                                                               VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                                 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                   I PKEQGVLSFWRGNLANVIRY FPTQALNFAFKDKYKQI FLGGVDKHTQFWRY FAGNLASG
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2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0693056
2000US-07273444
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Wehrman T, X
Goodrich R,
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Xu C,
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Pred. No. 1.4e-:
3; Mismatches
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Drmanac R
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Zhang J;
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                                                                                                                                                                                                                                                                                                                                       polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (BTM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention on treatment of diseases associated with altered mitochondrial function of dysfunctional cell survival, such as Alzheimer's disease, disbetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; canc alzheimer's disease; diabetes mellitus; hyperproliferative disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polymuclectide encoding MPT polypeptide or cyclophilin polypeptide
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Velicelebi G,
                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 186pp; English
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                           GAAGATSLCFVYPLDFARTRLAADVGKAGABRBFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           energy transfer molecule
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                                                                                                                                                                                                                                                              298 AA;
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G, Davis RB;
                                                                                                                                                                                             Conservative
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                                                               FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                           Score 1454; DB 22;
Pred. No. 1.4e-144;
3; Mismatches 9;
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                                                                                                                                                                                                                                                   comprising a regulated promoter operably linked to a nucleic acid comprising an adenine nucleotide translocator (ANT) polypeptide. ANT cancoling an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ANT synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant and polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Consider the polypeptide, or cells expressing the polypeptide. ANT considered in susful for determining the presence of an ANT polypeptide, and considered is useful for determining the presence of an ANT polypeptide, or preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating the present sequence a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                      Matches
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson (Ghosh SS,
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 2; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001; 2001WO-US15416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; adenine nucleotide translocator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adenine nucleotide translocator 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU10380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MITO-) MITOKOR.
                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-055598/07
                                                                                      274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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1 MTDAALSFAKDFLAGGVAAAISKTAVAAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CM, Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS16690.
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                                                                                                                                                                                                         298
                                                                                      Conservative
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                                                                                                                94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298
                                                                                   Score 1454; DB 23;
Pred. No. 1.4e-144;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression construct (I)
linked to a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for producing adenine nucleotide regulated promoter linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ANT3).
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                                                                                         Indels
                                                                                                                                           Length
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                                                                                      Gaps
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ARESULT 9
AAM41427
ID AAM4
AC 
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                             Tang
Wang
Zhao
                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000;
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                                                                                                                                                                                                                                                                                          AAI60583.
                                                                                                                                                                                                                                                                                                                                                          Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-0488725.
; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
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                                                                                                                                                                                                                                                                                                                                                          Asundi V, Ch
Wehrman T, X
Goodrich R,
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Xu C,
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Xue AJ,
mac RT;
                                                                                                                                                                                                                                                                                                                                                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                              treating
                                                                                                                                                                                                                                                                                                                                                                                                         Ren F,
                                                                                                                                                                                                                                              disorders
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                                                                                                                                                                                                                                                                                                                                                                                                         Wang
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous

Example

2; SEQ ID NO 6358; 10078pp; English

system, such as peripheral

nervous injuries, peripheral

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RESULT 10
ABG15423
ID ABG15423
XX ABG15423
AC ABG15
XX IB-FE
XX Homan
KW Homan
KW Food
XX Homo
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Best Local
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                       (HYSE-)
                                                                                                                                                                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002
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CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO construction of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.6%;
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Pred. No. 1.3e-140;
3; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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Best Local S
Matches 265
                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which removed the arm and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                       independent
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                                                                                                                                                                                                                                                                                                          Similarity 89.2
65; Conservative
                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                              VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPPDTVRRRMM 240
                                                                                                            GAAGATSLCFVYPLDFARTTLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                             I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                               I PKEQEVLS FWRGNLANVI RYF PTQALNFA FKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                        MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                        MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                           298
                                                                                                                                                                                                                                                                                                                                                                                                         of ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 39-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macgregor
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                                                                                                                                                                                                                                                                                                        91.2%; Score 1411; DB 19;
89.2%; Pred. No. 4.9e-140;
tive 15; Mismatches 17;
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B
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             297
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ABU53

14-APR-2003 ABU53219;

(first

entry)

Human adenine nucleotide translocator ANT1

29-AUG-2000 AAY71031,

(first entry)

RESULT 12

ABU53219

standard;

Protein;

293

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RESULT 13
AAY71031
ID AAY71
XX
AC AAY71
XX
AC AAY71
XX
DT 29-AU
XX
DB Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                     AAY71031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human metabolism-associated DKFZphtes3_35n12 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example III; Page 850; 1095pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-327840/34.
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28-SEP-1999;
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                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                               185
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                                                                                                                                                                                                                                                                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 264;
                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                QEVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG 124
                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                 QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG
                                                                                                                                                                             KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                    IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPPDTVRRRMMQSGR
                                                                                                                                                                                                                                                                          ATSLCFVYPLDFARTRLAADVGKGSSQRBFNGLGDCLTK1FKSDGLKGLYQGFSVSVQGI
                                                                                                                                                                                                                                                                                           ATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI
                                                                                                                                                                                                                  IIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMQSGR
                                                                                                                                                            KGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-IB01496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0149499
99US-0156503
                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1409; DB 22;
Pred. No. 7.7e-140;
5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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(ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, cleber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antiddabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 44; Page 172; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson CM,
Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patent discloses a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-365619/31.
DB; AAD00519.
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                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                                                                                                                                                                                        MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                                                             IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                       89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clevenger W,
                                                                                                                                                                                                                                                                                                                                                                         ; Score 1391.5;
; Pred. No. 5.5e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                          .5e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                       297;
                                                                                                                                                                                                                                                                                                                                                                         <u>,,</u>
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Query Match Best Local Similarity

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                                               regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GPP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. Those agents are useful for the prevention treatment of diseases associated with altered mitochondrial function dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                 The present sequence represents human adenine nucleotide translocator-I (ANT-1) protein. ANT proteins are mitochondrial permeability translation (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to with other mitochondrial core components e.g. cyclophilins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises golynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenine nucleotide translocator-1 (ANT-1) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01198
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                                 hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy AN, C:
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-NOV-2000; 2000WO-US30535.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clevenger W,
G, Davis RE;
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                                   disorders
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell an culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, is useful for determining the presence of an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 44; Fig 2; 147pp; English.
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N-PSDB; AAS16688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenine nucleotide translocator; ANT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenine nucleotide translocator 1 (ANT1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2000; 2000US-0569327
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DOS WH, Pei Y, Carroll AK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for producing adenine nucleotide regulated promoter linked to
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                                                                                                                                                                                                                                                                                                                                                                                      ANT from a biological sample, where the ANT ligand is covalently or non-
covalently bound to a solid phase. Detectably labeled ANT ligand is also
useful for identifying an agent that interacts with an ANT polypeptide.
The present sequence represents the amino acid sequence of human ANT1.
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                                                                                                                                                                                                                                       Similarity
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                 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKY 297
                                                                                                                                                                                                       IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                          VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRMM
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QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                         VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRWM
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Pred. No. 5.5e-138;
7; Mismatches 16;
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Search completed: December 18, Job time : 35.3729 secs 2003, 12:40:46

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Result
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-160-119-3
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US-09-160-119-3
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US-08-518-878B-51
US-08-93-75-0681A-51
US-08-93-15-681A-51
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/434,354; CURRENT FILING DATE: 1999-11-03; NUMBER OF SEQ ID NOS: 54; SOPTWARE: FASTSEQ for Windows Version 3.0; SEQ ID NO 48; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapien
US-09-434-354-48
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US-09-434-354-48
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1547; DB 4; Best Local Similarity 100.0%; Pred. No. 1.2e-169;
                                                                                                                                                                                                                                                                                                                                                                          Matches
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
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                                                                                           VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
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                                                                                                                                                                                                                          Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigerl, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi Gonul
APPLICANT: Davis, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 54
SOFTWARE: FRATSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
3-09-434-354-49
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Best Local Similarity
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Patent No. 6562563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND RUTITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                         NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                      CITY: Boulder
STATE: Colorad
                                                                                                                                                  STREET:
                                                             ZIP: 80303
                                                                                     COUNTRY:
                                                                                                                                                                   ADDRESSEE:
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                                                                                                      Colorado
                                                                                                                                                  5370 Manhattan Circle, Suite 201
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RESULT 4
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SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TYPE: amino acid
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Best Local Similarity 89:2%;
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APPLICATION NUMBER: US/08/961,871
FILLING DATE: 31-OCT-1997
CLASSIFICATION NUMBER: US 60/030,017
FILLING DATE: 31-OCT-1997
CLASSIFICATION NUMBER: US 60/030,017
APPLICATION NUMBER: US 60/030,017
APPLICATION NUMBER: US 60/030,017
FILLING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Perber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                            QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKY 297
                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM 240
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; Pred. No. 5.6e-154;
15; Mismatches 17;
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RESULT 4
US-09-434-354-47
US-09-434-354-7
Sequence 47, Application US/09434354
Patent No. 6565563
GENERAL INFORMATION:
APPLICANT: Miley, Anne N.
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miley, Sandra Eileen
APPLICANT: Heleyeri, Luciano G.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FC
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FC
TITLE REFERENCE: 660088 4.33
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT APPLICATION DAVE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien

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APPLICANT: Zhang, Zemin

ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FITTLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C13

CURRENT PILING DATE: 2001-11-14

FRIOR APPLICATION NUMBER: 05/049787

FRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-10-17

FRIOR APPLICATION NUMBER: 60/06250

FRIOR PILING DATE: 1997-11-12

FRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

FRIOR FILING DATE: 1997-11-23

FRIOR FILING DATE: 1997-11-24

FRIOR APPLICATION NUMBER: 60/06570

PRIOR APPLICATION NUMBER: 60/075945

FRIOR FILING DATE: 1997-11-24

FRIOR FILING DATE: 1997-11-27

FRIOR APPLICATION NUMBER: 60/075945

FRIOR FILING DATE: 1998-02-25
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US-09-996-243-289
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Grimaldi, J. Christopher
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Ferrara, Napoleone
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RAPPLICATION NUMBER: 60/089440

DR FILING DATE: 1998-06-16

PR PILICATION NUMBER: 60/089512

R FILING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089514

DR PILING DATE: 1998-06-16

OR APPLICATION NUMBER: 60/089532
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OR APPLICATION NUMBER: 60/088738
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088910
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OR APPLICATION NUMBER: 60/088924
OR PILING DATE: 1998-06-10
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FILING DATE: 1998-06-02
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FILING DATE: 1998-05-07
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FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17

NUMBER: 60/089599

APPLICATION NUMBER: 60/089801

ILING DATE:

1998-06-18

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089600

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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Wind
SEQ ID NO 339
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 86; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 339,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 61505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-07-09
126 TSLCFVYPLDFARTRLAADVGKAGAEREERGLGDCLVKIYKSDGIKGLYQGENVSVQGII 185 : | : | : | : | : | : | : | : | | 185
                                                            238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 LWRGNGINVLKIAPESAIKFMAYEQIKR--LVGSDQET---LRIHERLVAGSLAGAIAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                        188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM------CIVGGFTQMIREG
                                                                                                                                                                           10 KDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVV----RIPKEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
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                                                          GAKSLWRGNGINVLKIAPESAIKFMAYEOMKR--LVGSDQET---LRIHERLVAGSLAGA
                                                                                              EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QASIEGAPEVTMSSL--FKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDEIK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYFGIYDTAKGM-----LPDPKNTHIVISWMIAQTVTAVAG-LTSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRA
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                                                                                                                                                                                                                 Score 301; DB 3; I
Pred. No. 7e-26;
52; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 302; DB 4;
Pred. No. 5.4e-26;
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                                                                                                                                                                                                                                                       DB 3; Length 469
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APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252

APPLICATION NUMBER: 60/090355

LING DATE: 1998-06-23

APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907

LING DATE:

1998-06-18

LING DATE: 1998-06-19

APPLICATION NUMBER: 60/089952

1998-06-19

APPLICATION NUMBER: 60/090246

1998-06-22

LING DATE:

LING DATE: 1998-06-22

FILING DATE:

FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02

APPLICATION NUMBER: FILING DATE: 1998-07

NUMBER: 60/091519

1998-07-01

60/091544

FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/090862

FILING DATE:

1998-06-26 1998-06-25

APPLICATION NUMBER:

60/090696

LING DATE:

LING DATE: 1998-06-25

APPLICATION NUMBER: 60/090695

1998-06-25

60/090694

APPLICATION NUMBER: FILING DATE: 1998-06

LING DATE: LING DATE:

1998-06-25

APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090676

1998-06-25 1998-06-25

APPLICATION NUMBER: 60/091360

APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24

LING DATE:

APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090540

LING DATE:

LING DATE:

1998-06-24 1998-06-24 1998-06-24 1998-06-24

APPLICATION NUMBER: 60/090472

LING DATE: 1998-06-24

LING DATE:

ING DATE:

60/090535

PLICATION NUMBER: 60/090445

1998-06-24

APPLICATION NUMBER: 60/090435

1998-06-24 1998-06-24

PLICATION NUMBER:

60/090444

ING DATE:

PPLICATION NUMBER: 60/090431

ING DATE:

APPLICATION NUMBER:

LING DATE:

1998-06-23

60/090429

LING DATE:

1998-06-24

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RESULT 8
US-09-501-558-2
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
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US-09-312-283C-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin
TITLE OF INVENTION: And Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 TSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 GAKSLWRGNGINVLKIAPESAIKFMAYEOMKR--LVGSDOET----LRIHERLVAGSLAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM------CIVGGFTQMIREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339, Application US/09312283C
5. 6573095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYRAAYFGIYDTAKGMLPDPKNTHI------VISWMIAQTVTAVAG-LTSYPFDT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLK 461
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                                                                                                                                                                                                     NLK 461
                                                                                                                                                                                                                                                                                                       VRTRMQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYE
                                                                                                                                                                                                                                                                                                                                                                                                      PYAGIDLAVYETL------KNTWLQRYAVNSADPGVFVLLACGTISSTCGQLASYPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAOSSIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAKEGVAAFYKGYIPNMLGII
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Sleeman, Matthew
Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.5%; Score 301; DB 4; Length 469; 28.4%; Pred. No. 7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
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                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/92,922
EARLIER APPLICATION NUMBER: 60/92,922
EARLIER FILING DATE: 1998-07-15
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SOFTWARE: Fab
; SEQ ID NO 2
; SNGTH: 291
                                                                                                                                                 SEQ ID NO 118
LENGTH: 335
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Best Local Similarity
                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (335)
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APPLICANT: Sands, Archur T.
TITLE OP INVENTION: No. 6403784el Human Uncoupling Proteins
TITLE OP INVENTION: Polymucleotides Encoding the Same
FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
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APPLICANT:
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TITLE OF INVENTION: 71 Human Secreted Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 SGGAAGATSLCEVYFLDFARTRLAADVGKAGABREFRGLGDCLVKIYKSDGIKGLYQGFN 178
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Mathur, Brian
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27.8%; Pred. No. 4.3e-23;
live 55; Mismatches 134;
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US-09-160-119-4
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US-09-482-273-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KRIEF, STEPHANE
APPLICANT: BRIL, ANYOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: HOMO SAPIENS
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No. 6316219
INFORMATION:
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                     KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGG-AFVLVLYDEIKKY 297
                                                              AIYFPCYAHVKASFANEDGQVSPGSLLLA---GAIAGMPAASLVTPADVIKTR--LQVAA 324
                                                                                                       AAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTS----YPFDTVRRRMMQSGR
                                                                                                                                                IFTNPLEIVKIRLQV----AGBITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFS
                                                                                                                                                                                                                                RGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAGGCAGGSQV
                                                                                                                                                                                                                                                                       RGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKRTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                              FGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 163
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7; Pred. No. 5.4e-23;
51; Mismatches 134; Indels
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US-09-160-119-2
Sequence 2, Application US/09142565A Patent No. 6187560
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LENGTH: 674
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FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
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                                                                                                                                                                                                                                                                                                             443 IFTNPLEIVKIRLQV-----ÄGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFS 496
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                                                                                                                                   RAGOTTÝSGVIDČERKÍLKEEGPKALWKGAGARVERSSPOEGVTLLTYELLORW
                                                                                                                                                                                                                         AIYPPCYAHVKASFANEDGQVSPGSLLLA---GAIAGMPAASLVTPADVIKTR--LQVAA
                                                                                                                                                                                                                                                                                                                                                                                               RGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAGGCAGGSQV 442
                                                                                                                                                                         KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNYLRGMGG-AFVLVLYDEIKKY 297
                                                                                                                                                                                                                                                                AAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTS----YPFDTVRRRMMQSGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.9%; Score 261.5; DB 4 ilarity 26.2%; Pred. No. 4.4e-21; Conservative 51; Mismatches 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICHEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Mismatches 139;
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551

FITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-07-16

GENERAL INFORMATION:

APPLICANT: Lee James Beeley APPLICANT: Kelly Paine APPLICANT: Robert James

SEQ ID NO 2

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US-08-775-009-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08775009 Patent No. 5935783
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Best Local Similarity
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TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REGISTRATION NUMBER: CH-0681
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1396
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                            TELEPHONE:
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                                                                                                            (215) 568-3100
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US-08-518-878B-51
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Best Local Similarity
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                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Tartag
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,87/
FILLING DATE: 23-AUG-1995
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                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                          NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY:
                                                LENGTH:
                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 YRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSY----PFDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 SLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIII 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51, Application US/08518878E
5. 5702902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LYRGLSSLLYGSIPKAAVRFGMFEPLSNHMRDAQGRLDSR------RGLLCGLGAGVAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 KAILAGGLAGGIBICITFPTBYVKTQLQLDERAN----PPRYRGIGDCVRQTVRSHGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 KDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
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                                                 309 amino acids
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ilarity 28.1%;
Conservative (
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unknown
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                single
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TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                 US/08/518,878B
                                                                                                                                                                                            30,742
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                                                                                                                                                                              7853-036
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Pred. No. 1.2e-19;
7; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND METHODS FOR THE
BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                                                                                                      Version
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Length 309;

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RESULT 15
US-08-807-861A-51
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 ami-
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                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atent No. 5853975
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tartaglia, CITLE OF INVENTION: MITTLE OF INVENTION: RI
                                                                                                                                                       NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 26-FEE CLASSIFICATION: 514
                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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5853975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVRRRWWMQS-GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSVQGIIIYRAAYFGIYDTAX-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFD
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                                                                                                (212) 869-9741/8864
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METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/807,861A
                                                                                                                                                           7853-066
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; TOPOLOGY: unb
US-08-807-861A-51
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 291
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                                                                        237 VVKTRYMNSALGQ-----
                                                                                                          233 TVRRRMMOS-GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVL
                                                                                                                                               181 PNVARNAIVNCABLVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVD
                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                              67 LTMVRTEGPRSLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHAS-----IGSRLL 121
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                                    YDBIKK 296
                                                                                                                                                                                 VSVQGIIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFD 232
                                                                                                                                                                                                                     AGSTTGÁLAVAVAQPTDVVKVRFQÁQ-ARÁĞGGRRYQSTVNAYKTI AREEĞFRĞLWKĞTS
                                                                                                                                                                                                                                                                                                                                  VRIPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLA 118
YEQLKR 296
                                                                                                                                                                                                                                                        SGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFN 178
                                                                                                                                                                                                                                                                                                                                                                      TDVPPTATVKFLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                           15.5%; Score 239.5; DB 2;
23.5%; Pred. No. 4.4e-19;
Live 58; Mismatches 149;
                                                                          - YSSAGHCALTMLQKÉGPRÁFYKGFMPSFLRLGSWNVVMFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 309;
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Search completed: December 18, 2003, 12:44:55 Job time : 13.3471 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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1547
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11:
12:
13:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:
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2284.595 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

		Result No.
5 1454 7 1391.5 8 1391.5 9 1391.5 9 1391.5 1 779.5 2 752.5 2 752.5 4 741.5 734	1 1547 2 1547 2 1547 3 1547 4 1454	. Score
94 444 55 50 60 60 60 60 60 60 60 60 60 60 60 60 60	100.0	Query Match
298 298 297 297 179 301 318 381 381	298 298 298 298	t Query Match Length
9 9 10 12 12 12 15	910	DB
US-09-810-644-33 US-09-185-904A-33 US-09-811-094-31 US-09-810-644-31 US-09-185-904A-31 US-10-029-386-32501 US-10-032-585-7194 US-10-032-585-7194 US-10-141-478A-2 US-10-141-478A-2 US-10-141-478A-2 US-10-141-478A-3338	US-09-811-094-32 US-09-810-644-32 US-09-185-904A-32 US-09-811-094-33	ID
Sequence 33, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 3501, A Sequence 32501, A Sequence 252, Appl Sequence 252, Appl Sequence 270, Appl Sequence 170, App Sequence 3338, Ap	Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 33, Appl	Description

45 302	44 302	43 302	42 302		40 302					35 302	34 302	33 302	32 302	31 302	30 302	29 302	w	w	26 302	25 302	24 302	w	22 323.5		ı	19 448	18 484	17 677.5	
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US-09-997-653-289	US-09-989-734-289	US-09-993-687-289	US-09-990-436-289	US-09-989-730-289	US-09-991-181-289	US-09-990-444-289	US-09-989-735-289	US-09-989-293A-289	US-09-992-598-289	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	US-09-989-732-289	US-09-989-731-289	US-09-989-727-289	US-09-989-279-289	US-09-989-723-289	US-09-989-722-289	US-10-094-749-1789	US-09-777-921A-5	US-09-777-921A-4	US-09-777-921A-2	US-09-864-761-36440	US-09-925-301-1459	US-10-259-165-192	** ** *** ***
Sequence 289, App	289,	•	Sequence 289, App	289,	289,		Sequence 289, Ap	289,	•	289,	289,	289,	289,	289,	289,	289,	e 289		289,	289,	Sequence 289, App	17	ŗ	4	Sequence 2, Appli	364	1459,		de la contraction de la contra

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; Sequence 32, Application US/09811094
; Patent No. US20010044144A1
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                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32
                                                                                                                                        Query Match
Best Local Similarity
Matches 298; Conserv
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
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TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
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                                                                                1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
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Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
                                                        MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
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                                                                                                                                                                                   Length 298;
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; Sequence 32, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
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US-09-185-904A-32
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US-09-810-644-32
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
S-09-810-644-32
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Patent No. US20020012992A1
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Best Local Similarity
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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; SOFTWARE: FastSEQ for I
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32
                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
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US-09-811-094-33
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US-09-811-094-33
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          TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 66008.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRANTSEQ for Windows Version 3.0
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
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Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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: Willer, Scott W.
: Szabo, Tomas R.
: Glabh, Soumitra S.
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Query Match Best Local Similarity

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Score 1454; DB 9; Pred. No. 7.7e-149;

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 33
LENGTH: 298
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APPLICANT: Davis, Ro
APPLICANT: Clevenger,
APPLICANT: Wiley, Sar
APPLICANT: Willer, Sc
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                                                                                                                                                                                                                                                                                                                                   Query Match 94.0%; Score 1454; DB 9; Length Best Local Similarity 92.6%; Pred. No. 7.7e-149; Matches 274; Conservative 13; Mismatches 9; Indels
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
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ORGANISM: Homo sapien
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5. US20020012992A1
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                     QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                                                  VQGIIIYRAAYEGVYDTAKGMLEDEKNTHIVVSMMIAQTVTAVAGVVSYEEDTVRRRMM
                                                                                                    VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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Moos, Walter H.
Pei, Yazhong
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APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Grabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASS, TILE REFERENCE: 660088,420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILNG DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
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US-09-811-094-31
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; ORGANISM: Homo
US-09-185-904A-33
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US-09-185-904A-33
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APPLICANT: Anderson,
APPLICANT: Davis, Rob,
APPLICANT: Clevenger,
APPLICANT: Wiley, San,
APPLICANT: Willer, Sc,
APPLICANT: Szabo, Tom
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APPLICANT: Anderson, Christe
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, Willi
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Best Local Similarity
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CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Clevenger, William
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Pred. No. 7.7e-149;
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; ORGANISM: Homo
US-09-811-094-31
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SEQ ID NO 31
LENGTH: 297
                                                                                                                                                           Query Match
Best Local Similarity 88.6
'-- 263; Conservative
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 31
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APPLICANT:
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Patent No. US20020012992A1
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ORGANISM: Homo sapien
-09-810-644-31
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                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
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GAAGATSLCFYYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                  IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                            MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                          MGDHAWSFLKDFLAGAVAAAVSKTAVAPIBRVKLLLQVQHASKQISABKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                         Ghosh, Soumitra S. Moos, Walter H. Pei, Yazhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clevenger, William Wiley, Sandra Eileen Willer, Scott W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.9%;
                                                                                                                                                                                      89.9%; Score 1391.5; DB 9
88.6%; Pred. No. 4.5e-142;
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Pred. No. 4.5e-142;
                                                                                                                                                                        Mismatches
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RESULT 10
US-10-029-386-32501
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                          Sequence 32501, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT K.
APPLICAN
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Best Local Similarity
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SEQ ID NO 31
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Patent No. US20020177185A1
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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REFERENCE: AEOMICA-X-2
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pred. No. 4.5e-142;
L7; Mismatches 16; I
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US-10-032-585-7194
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US-10-032-585-7194
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 7194
LENGTH: 301
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SEQ ID NO 32501
LENGTH: 179
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 1018-2005-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN BUILT, LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 54.3%;
Local Similarity 98.8%;
                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRAAYFGIYDTAKG 200
  178
                                                                                   120
                                                                                                                             59
                                                                                                                                                                                                                                                                                                 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161;
                                                                                                                                                                     60
                                                                                                                                                                                                           Similarity
                                                                                                                           RTAADEGVVSFWRGNTANVIRYPPTQALNFAFKDKFKAMF--GFKKDENYWKWFAGNLAS 116
                                                                        GGAAGATSLCFVYPLDFARTRLAADV--GKAGAEREFRGLGDCLVKIYKSDGIKGLYQGF 177
                                                                                                                                                      RIPKEQEVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I PLGGVDKRTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFLGGVDKRTQFWLYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGL 120
NVSVQGIIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRR 236
                                       GGLAGATSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRAAYFGIYDTAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQHASKQITADKQYKGIIDCVVRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                50.4%;
                                                                                                                                                                                                                                                                                            ; Score 779.5; DB 12; Length 301; ; Pred. No. 8e-76; 41; Mismatches 84; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 840; DB 12;
Pred. No. 1.1e-82;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                            Gaps
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RESULT 13
US-10-141-478A-2
; Sequence 2, Application US/10141478A
; Publication No. US20030148300A1
; GENERAL INFORMATION:
; APPLICANT: Valentin, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-801-368-252
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US-09-801-368-252
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LENGTH: 318
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Best Local (
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
FRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 10500-01-19
PRIOR FILING DATE: 10500-01-01
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
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Local Similarity 54.3%;
tes 159; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 EVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 NFLIDFLMGGVSAAVAKTAASPIERVKLLIQNQDEMLKQGTLDRKYAGILDCFKRTATQE 81
                                                                                                                                                                                                                                                                                                                                                                                                                       82 GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF--GFKKEEGYAKWFAGNLASGGAAGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQ-HASKQITADKQYKGIIDCVVRIPKEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holtzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
No. US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                                      TSLCFVYPLDFARTRLAAD--VGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYMMYTSGQA---VKYDGALDCFRKVVAAEGVGSLFKGCGANILRGVAGAGVISLYDQLQ 292
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                                                                                                                                                                                                                                                                                 IIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLISYPFDTVRRRMMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salama, Sofie
Sherman, Amir
Silva, Jeff
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                                                                                                                                                                    GQA----VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQ 309
                                                                                                                                                                                                                                                       IVVYRGLYFGMYDSLKPLLLTGSLEGSFLASFLLGWVVTTGASTCSYPLDTVRRRMMTS
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Hecht, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 752.5; DB 10; Length 318; Pred. No. 7.2e-73; 40; Mismatches 85; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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RESULT 14
US-09-734-569-170
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Best Local Similarity 53.6%;
Matches 165; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                Sequence 170, Application US/09734569 Patent No. US20020064816A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Moss genes from Physcomitrella patens TITLE OF INVENTION: In the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101
                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/141,478A
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,527
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
PRIOR PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
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APPLICANT: Zang, Wei
APPLICANT: Zang, Wei
TITLE OF INVENTION: Metabolite Transporters
                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VQGIIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GATSLCFVYPLDFARTRLAAD----VGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EQEVLSFWRGNIANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNIASGGAA 123
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                                                                                                                                                                                                                                                                                   Lerchl, Jens
Renz, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIVEGRACY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRMMQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEI-
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                                                                                                               Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
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Voelker, Toni
                                                                                                                                                                       Freund, Annette
                                                                                                                                                                                             Frank, Markus
                                                                                                                                                                                                               Bischoff, Friedrich
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Pred. No. 1.4
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                                                                                               proteins
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7 SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITA---DKQYKGIIDCVVRIPK 63

Indels

12;

Gaps

Matches

157;

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                                                                                         ; ORGANISM: Aspergillus fumigatus US-10-128-714-3338
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US-10-128-714-3338
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                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 3338
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 181
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 170
LENGTH: 386
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.9%;
Best Local Similarity 53.4%;
                                          Query Match
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APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
FILE REFERENCE: 10182-018-999
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
                                                                                                                                  LENGTH: 30
TYPE: PRT
                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/295,890 PRIOR FILING DATE: 2001-06-05 PRIOR APPLICATION NUMBER: US 60/303,899 PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/316,362
                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 TSLCFVYFLDFARTRLAADV---GKAGABRBFRGLGDCLVKIYKSDGIKGLYQGFNVSVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 GIIIYRAAYFGIYDTAKG-MLPDFKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 SSLLFYYSLDYARTRLANDAKSSKKGGGERQFNGLVDVYKKTLATDGIAGLYRGFAISCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA
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                       Similarity
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47.4%; Score 734; DB 15; 53.2%; Pred. No. 6.9e-71; ive 41; Mismatches 85;
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Pred. No. 1.5e-71;
12; Mismatches 86;
                                            Length 308;
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	Search completed: December 18, 2003, 12:55:43 Job time : 24.3606 secs	arch comple o time : 24	Sea
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	241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGWGGAFVLVLYDEIK 295	241	Ş
243	LGIVVYRGLYFGMYDSIKEVVLVGSLEGSFLASFLLGWTVTTGAGIASYFLDTIRRRMM	184	ઠ
240	182 QGIIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPPDTVRRRMM 240	182	\$
183	124 GATSLLFVYSLDYARTRLANDAKSAKGGGERQFNGLIDVYRKTLASDGTAGLYRGFGPSV	124	뮹
181	124 GATSLCEVYPLDEARTRLAADVGKAGABRBFRGLGDCLVKIYKSDGIKGLYQGFNVSV 181	124	Ş
123	65 AEGVMSLWRGNTANVIRYFTQALNFAFRDTYKSMFAYKKD-RDGYAKMMMGNLASGGAA 123	65	용
123	64 EQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAA	64	Ş
64	7 AFTDSFAVGGVSAAVSKTAAAPIERIKLLVQNQDEMIRAGRLDRKYNGIIDCFRRTAQ	7	용

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1547
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/cgm2_6/ptodata/1/paa/US106_COMB.pep;*
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gn2_6/ptodata/1/paa/US083_COMB.pep:*
gn2_6/ptodata/1/paa/US084_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ц	Result No.
1547	sult Query No. Score Match Length DB ID
100.0	Query Match
298	Length D
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1 1547 100.0 298 1 PCT-US01-15416-32 Sequence 32, Appl	ID
Sequence 32, Appl	Description

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-09	-389-987-	10-408-765A-168	US01-08631-4	-60-412-418-239	-60-389-987-239	-10-408-765A-23	Ϋ́	-10-403	-10-286-897-6	-10-258-898A-635	-488-725A-	-286-897-2	-10-258-898A-	-09-811-	-09-811-094-3	-09-810-644-3	-09-809-889-3	-09-809-827-3	09-709-785-	-09-569-	09-488-725A	-09-393-441-3	09-18	-US01-15416-	-10-216	-09-760	US-60-412-418-1631	-60-389-987-1631	US-10-408-765A-1631	-10-316	-60-452-680-202	-10-466-162-54	-09-569-327-	-US02-01048-5	9-811-132-	094-3	-09-810-644-3	-09-809-889-3	US-09-809-827-32	US-09-709-785-48	US-09-393-441-32	-09-185-904A-
16	e 1680,	e 1680,	45782,	e 2398,	e 2398,	e 2398,	equence 15	e 154,	equence 6358,	O	e 6358,	e 2786	e 2786	33,	33,	33,	ω ω ,	33,	49	6, 2	2786	33	e u	33,	e 13:	e 1310,	1631,	e 1631	Sequence 1631. Ap	1767	98707	54	e 5, Appl	54,	e 32	e 32,	e 32,	e 32,	e 32,	e 48,	Sequence 32, Appl	e 32,

ALIGNMENTS

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ORGANISM: Homo sapien	TYPE: PRT	LENGTH: 298	SEQ ID NO 32	SOFTWARE: FastSEQ for Windows Version 3.0	NUMBER OF SEQ ID NOS: 48	CURRENT FILING DATE: 2001-05-11	CURRENT APPLICATION NUMBER: PCT/US01/15416	FILE REFERENCE: 660088.443PC	TITLE OF INVENTION: THEREFOR	TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING	TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE	APPLICANT: Ghosh, Soumitra S.	APPLICANT: Szabo, Tomas R.	APPLICANT: Willer, Scott W.	APPLICANT: Wiley, Sandra Eileen	APPLICANT: Clevenger, William	APPLICANT: Davis, Robert E.	APPLICANT: Anderson, Christen M.	APPLICANT: MitoKor	GENERAL INFORMATION:	Sequence 32, Application PC/TUS0115416	PCT-US01-15416-32	RESULT 1

ASSAYS

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; SOFTWARE: FastSEQ for P
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
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APPLICANT:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                            Local Similarity
 241
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                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.
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 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                                      I PKEQEVL SFWRGNLANV I RYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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Ghosh, Soumitra S.
VENTION: PRODUCTION OF ADENINE NUCLECTIDE
VENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Willer,
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Clevenger, William
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Pred. No. 2.9e-159;
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Pred. No. 2.9e-159;
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; ORGANISM: Homo sapien
US-09-393-441-32
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US-09-393-441-32
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SOFTWARE: Fabr
SEQ ID NO 32
FRIGTH: 298
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GENERAL I
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Velicelebi, Gomul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FO
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433C1
CURRENT FILLING DATE: 2002-09-16
CURRENT FILLING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                   APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
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CURRENT APPLICATION NUMBER: US/09/393,441
CURRENT FILING DATE: 1999-09-08
NUMBER OF SEQ ID NOS: 37
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Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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Pred. No. 2.9e-159;
Mismatches 0;
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; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-809-827-32
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US-09-809-827-32
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; ORGANISM: Homo
US-09-709-785-48
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LENGTH: 298
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/809,827
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 37
NOTENARE: PastSEQ for Windows Verbion 3.0
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APPLICANT: Davis, R
APPLICANT: Clevenge
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                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
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                                                             I PKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                           MTDAALSFAKDFLAGGVAAAISKTAVAPIBRVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clevenger, William Wiley, Sandra Eileen Willer, Scott W.
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Pei, Yazhong
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                                                                                                                                                                                      100.0%; S illarity 100.0%; F Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christen M.
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                                                                                                                                                                                       Score 1547; DB 23;
Pred. No. 2.9e-159;
); Mismatches 0;
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Pred. No. 2.9e-159;
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RESULT 7 US-09-810-644-32

Sequence 32, Application US/09810644 GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.

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CURRENT APPLICATION NUMBER: US/09/809,889
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapien
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Wiley, Sandra Elleen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
                                                                                              VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVK1YKSDGIKGLYQGFNVS 180
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
                              QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 201-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRANKSEQ for Windows Version 3.0
SEQ ID NO 32
ENGINE 298
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                                                                   Matches 298;
                                                                                   Query Match
Best Local Similarity
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                                                                                                                                          ORGANISM: Homo sapien
-09-811-094-32
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING FILE REFERENCE: 660088.420D4
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                                                                                                                                                                             TYPE: PRT
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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                       MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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MTDAALSFAKDFLAGGVAAAISKTAVAFIERVKLILQVQHASKQITADKQYKGIIDCVVR 60
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Clevenger, William
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Conservative (
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                                                                   Score 1547; DB 23;
Pred. No. 2.9e-159;
; Mismatches 0;
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Pred. No. 2.9e-159;
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D5
CURRENT APPLICATION NUMBER: US/09/811,132
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
RCANISM: Homo sapien
US-09-811-132-32
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US-09-811-132-32
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APPLICANT:
APPLICANT:
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Local Similarity 100.0%;
les 298; Conservative 0
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willer, Scott W.
szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
                                                                                            VQGIIIYRAAYFGIYDTAKGMLPDFKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                     QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAMSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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Pred. No. 2.9e-159;
); Mismatches 0;
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RESULT 10 PCT-US02-01048-54

Sequence 54, Application PC/TUS0201048 GENERAL INFORMATION: APPLICANT: EXLIXIS, INC.

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US-09-569-327-5
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                                                                                                                      US-09-569-327-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09569327 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-01-11
Prior Application removed - See File Wrappe
NUMBER OF SEQ ID NOS: 76
SOPTWARE: Patentin version 3.1
SEQ ID NO 54
                                                           Query Match
Best Local Similarity
Matches 296; Conserv
                                                                                                                                                                               SEQ ID NO 5
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                                                                                                                                                                                                                                                     TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LITLE OF INVENTION: AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.443
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, APPLICANT: Davis, Ro
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                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/569,327
CURRENT FILING DATE: 2000-05-11
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APPLICANT:
                                                                                                                                 LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapiens
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Similarity 99.3%;
96; Conservative
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYT 298
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Carroll, Amy K.
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Miller, Scott W.
Szabo Tomas R.
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Moos, Walter H.
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                                                           Conservative
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                                                                        99.4%;
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                                                         Score 1537; DB 19;
Pred. No. 3.5e-158;
1; Mismatches 1;
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Pred. No. 3.5e-158;
1; Mismatches 1;
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; ORGANISM: Homo sapiens
US-10-466-162-54
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US-10-466-162-54
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PRIOR PILLING DATE: 2001-01-12
PRIOR PELLICATION NUMBER: US 60/261,361
PRIOR PILLING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,531
PRIOR PILLING DATE: 2001-01-12
PRIOR PILLING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,457
PRIOR PILLING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,226
PRIOR PILLING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR PILLING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR PILLING DATE: 2001-01-12
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LENGTH: 298
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           Matches
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CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US 60/261,335
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,694
PRIOR APPLICATION NUMBER: US 60/261,694
PRIOR FILING DATE: 2001-01-12
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TITLE OF INVENTION: Modulating Insulin Receptor Signaling
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VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
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Pred. No. 3.5e-158;
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RESULT 14

US-09-760-469-1767

Sequence 1767, Application US/09760469

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PTZ54

CURRENT APPLICATION NUMBER: US/09/760,469

CURRENT FILING DATE: 2001-01-16

CURRENT FILING DATE: 2001-01-16
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES
FILE REPERENCE: CL001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH. 2008
                                                                                                                                              Prior application data removed -
NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                    LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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-60-452-680-20286
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TYPE: PRT
                 LOCATION: (8)
OTHER INFORMATION:
                                                        NAME/KEY:
NAME/KEY: SITE
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                                                          SITE
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                   Xaa
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                 equals
                 any
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Pred. No. 3.5e-158;
                                                                                                                                                                                                           consult PALM
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                 of the naturally occurring
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RESULT 15
US-10-216-583-1767
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                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR APPLICATION NUMBER: 60/218,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/760,469
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                  SOFTWARE: Patentin Ver.
SEQ ID NO 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1767, Appli GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/216,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PTZ54C1N
                                                                                         PEATURE: misc_feature
                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                       LOCATION: (8) TOTHER INFORMATION: Xaa
NAME/KEY: misc_feature
LOCATION: (11)
                                        FEATURE
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nes 296; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
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Pred. No. 4.1e.
1; Mismatches
                                                         any of the naturally occurring L-amino
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NTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match	99.4%; Score 1537; DB 28; Length 332;
Matches 296	vative 1
Qy 1	MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
Db 35	MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 94
Оу 61	IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
95	IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 154
121	GAAGATSICFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
155	GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 214
Qy 181	VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLISYPFDTVRRRMM 240
215	VQGIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRWMM 274
Qy 241	QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGWGGAFVLVLYDEIKKYT 298
275	QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAMSNVLRGMGGAFVLVLYDEIKKYT 332

Search completed: December 18, 2003, 12:53:25 Job time : 166.852 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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PIR 76:*
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Gapop 10.0 , Gapext 0.5
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1547
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	. 15	14	13	12	11	10	9	8	7	0	ű	4.	ω	b	1	No.	Result
746	749.5	749.5	752	752.5	753	754	757	759	759	761.5	765	7	771	938	968	986	1029	1029	1032	1170	1413	1417	1417	1419	1454	1458	1479	1547	Score	
48.2	48.4	48.4	٠	8	8	48.7		49.1	•	49.2	•									75.6		•		91.7	•	94.2		100.0	Match I	Query
306	306	305	386	318	387	386	313	387	326	307	308	322	386	301	339	300	313	313	300	301	298	298	298	298	298	298	298	298	Length I	
N	N	N	N	_	N	N	۲	N	N	N	۳	N	N	N	N	N	N	N	N	_	Н	N	N	H	μ	N	N	μ,	BB	
T42011	T20012	S68154	S21974	A31978	S16568	S17917	XWNC	S14876	T25728	A36582	S30259	T40526	T09709	851132	A41677	T15206	T25850	T23207	T25371	S31935	A44778	160173	837210	XWBO	803894	B43646	S31814	A29132	Ħ	
ADP, ATP carrier pr	tical pro	ADP, ATP carrier pr		ADP, ATP carrier pr	ADP, ATP carrier pr	carrier		carr	tical pro	carr:	ADP, ATP carrier pr	adp/atp translocas	ATP	carrier	ú.				tical pro	ier	ADP, ATP carrier pr		ADP, ATP carrier pr	ADP, ATP carrier pr	ADP, ATP carrier pr	, ATP	P carrier	ADP, ATP carrier pr	Description	

4.4	42	4 4	သ သ	36	3 3	33	30
5	43	1 0	9	37	5	33	
334	350	372	388	665.5	741.5	745	746
322.5	340	356	372	521.5	728	741.5	745.5
21.6	22.6	24.0	25.1	43.0	47.9	48.2	48.2
	22.0	23.0	24.0	33.7	47.1	47.9	48.2
348	475	415	325	298	386	382	379
332	358	352	381	327	309	379	385
NN	ผผ	ผผ	N N	NN	NN	NN	- 2
D84798	T50686	T48171	T04273	T24029	S14874	S33630	T04608
T47703	T45934	T01729	T51158	T51577	A24849	S21313	S29852
probable mitochond	peroxisomal Ca-dep	hypothetical prote	hypothetical prote	hypothetical prote	ADP,ATP carrier pr	ADP,ATP carrier pr	ADP,ATP carrier pr
Ca-dependent solut	hypothetical prote	mitochondrial solu	hypothetical prote	ADP/ATP translocas	ADP,ATP carrier pr	ADP,ATP carrier pr	ADP,ATP carrier pr

ALIGNMENTS

					*
8	Db Qy	B &	B 8	Query M Best Lo Matches	RESULT 1 A22132 ADP,ATP car N,Alternate C;Species: C;Accession R;Battini, J,Biol. Ch A;Title: Mo A;Reference A;Accession A;Molecule A;Residues: A,Cross-ref R;Houldswor Proc. Natl. A;Title: Tw A;Reference A;Residues: A,Cross-ref R;Houldswor Proc. Natl. A;Title: Tw A;Reference A;Residues: A,Cross-ref R;Houldswor Proc. Natl. A;Reference A;Residues: A,Cross-ref A;Reperimen C;Genetics: A;Gross-ref A;Genetics: A;Gross-ref A;Genetics: A;Gross-ref A;Asp posit A;Cross-ref A;Asp posit A;Note: the C;Superfami C;Superfami C;Superfami C;Superfami C;Superfami C;Superfami C;Superfami C;Superfami C;Superfami C;Superfami
181 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM 240	121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180 	61 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120 	1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60 	Query Match 100.0%; Score 1547; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 4e-130; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 1 ADP,ATP carrier protein T2 - human N,Alternate names: mitochondrial ADP,ATP translocase 2 C;Species: Homo sapiens (man) C;Becies: Homo sapiens (man) C;B

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A;Molecule type: mRNA
A,Residues: 1-298 <POW>
A),Residues: 1-298 <POW>
A),Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; PiD:g529417
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...., Cattler protein T2 - mouse
N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: S31814
                                                                                                                                                                 Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
A;Status: preliminary
                                                                                                                                                                                                                                                                                  B43646
ADP, ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C;Accession: B43646
C;Accession: B43646
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
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submitted to the EMBL Data
A;Reference number: S31814
A;Accession: S31814
A;Status: preliminary
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$31814
ADP,ATP carrier protein T2
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F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-298 < COS>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGSKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTLVAGLTSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I PKEQGVLSFWRGNLANVI RYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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Pred. No. 4.5e-124;
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A;Residues: 1-298 <COZ>
R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed at A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP,ATP carrier protein T3 - human
N;Alternate names: ADP,ATP carrier protein T2
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT> F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes f
A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Accession: S03894
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000
C;Accession: S03894; B28116
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A; Residues: 1-298 <CC
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                                                                                                                                                          Matches 274;
                                                                                                                                                                                                   Query Match
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Best Local :
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                                                                                                          1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                                                                                Similarity
IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
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                                                                                                                                                          Conservative
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92.6%;
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                                                                                                                                                        Score 1454; DB 1;
Pred. No. 7.6e-122;
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W,Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646, S.M.; Runswick, M.J.; Walker, J.E.
B;Cowell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
                                  A; Description: catalyzes the exchange between cytosolic ADP and mitochondrial A; A; Note: located in the inner mitochondrial membrane C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein; bnp, ATP carrier protein; methylated amino acid, r; S-99/Domain: ADP, ATP carrier protein repeat homology <ACP1> F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP2> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP2> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP2> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP2> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3> F; 207-298/Domain: ADP, ATP Carrier F; 207-298/Domain: ADP, ATP Carrier F; 207-298/Domain: ADP, ATP Carrier F; 207-298/Dom
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A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
A; Note: residue 52 may be methyllysine
R; Babel, W.; Wachter, E.; Aquila, H.; Klingenberg,
Biochim. Biophys. Acta 670, 176-180, 1981
A; Title: Amino acid sequence determination of the J
A; Reference number: A61343; MUID: 82046808; PMID: 62:
A; Accession: A61343
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A;Residues: 208-298 < RAS>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A;Cuss-references: A;State Complete amino acid sequence of the ADP/ATP carrier
A;Reference number: A03181; MUID:82188267; PMID:7076130
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A;Cross-references: GB.M24102; NID:g529414; PIDN:AAA30768.1; R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two diac, Reference number: A24822; MUID:86295775; PMID:3017341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 49-63; 154-168 < OET>
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R;Laplace, C.; Costet, P. submitted to the EMBL Data A;Reference number: S37210 A;Accession: S37210
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N;Alternate names: adenine nucleotide carrier
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; Keywords: duplication; transmembrane protein; Keywords. ADP,ATP carrier protein repeat homology <ACP1>;19-9/Domain: ADP,ATP carrier protein repeat homology <ACP2>;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                            GAAGATSLCFVYFLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
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                                                QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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Pred. No. 1.5e-118;
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adenine nucleotide translocator - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #sequence_revision 02-Aug C;Accession: I60173
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Te Biochim. Biophys. Acta 1152, 192-196, 193 A;Title: Isolation and characterization of cD A;Reference number: I60173; MUID:94002161; PM A;Accession: I60173
A; Residues: 1-298 <LIA>
A; Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1;
R; Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A; Title: DNA sequences of two expressed nuclear genes for hum A; Reference number: S03893; MUID:89236396; PMID:2541251
A; Accession: S03893
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-298 <COZ>
                                                                                                                                                                                                                                                                                            A,Title: A human muscle adenine nucleotide translocator gene has four exons, A,Reference number: A44778; MUID:89340499; PMID:2547778
A,Accession: A44778
                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: mitochondrial ADP,ATP translocase 1
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A44778; S03893; A39891; A28116
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.
J. Biol. Chem. 264, 13998-14004, 1989
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F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Residues: 1-298 <RES>
A;Cross-references: EMB
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                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP, ATP carrier protein T1 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
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Pred. No. 1.5e-118;
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k;Neckelmann, N.; L1, K.; Wade, R.P.; Shuster, R.; Wallace, D.C. Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891
                                                                                                                                                                                                                                                                                                                                                       RESULT 9
S31935
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A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: A28116
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat h
                                                                                                                                                                                                                                                            ADP,ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4q35-4q35
(C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Superfamily: ADP,ATP carrier protein #status predicted <MAT>
F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACPl>
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A;Molecule type: DNA
A;Residues: 1-301 <BEA>
                                                                                                                                                       submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier A;Reference number: S31935 A;Accession: S31935
                                                                                                                                                                                                                                               R; Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
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A;Residues: 1-37 <HOU>
A;Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1;
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R; Houldsworth, J.; Attardi, G.
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265; Conserv
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Pred. No. 3.4e-118;
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C;Species: Ca
C;Date: 15-Oc
C;Accession:
R;Lloyd, C.
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T25371
T25371
T25371
hypothetical protein T27E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Ctt-1999 #sequence_revision 15-Oct-1999 #t.
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A;Introns: 20/1; 41/3; 115/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021;
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A;Reference number: Z20024
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Best Local Similarity
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                        TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKY 297
                                                                                                  RAAYFGIYDTAKGML-PDFKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQSGRKG
                                                                                                                                                                    LCFVYFLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
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                                                                                                                                               LCFVYPLDFARTRLAADIGKAN-DREFKGLADCLIKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                       AALWRGNLANVIRY PPTOAMNFAPKDTYKAI FLEGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                               FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMDVLIRVPKEQGV
                                                                                                                                                                                                                                                                                                                  FAKDFLAGGVAAAISKTAVAFIERVKLLLQVQHASKQITADKQYKGIIDCVVRIFKEQEV
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   -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDBIQKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone
                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
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78.1%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                   34;
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                                                                                                                                                                                                                                                                                                                                                                   Score 1032; DB 2;
Pred. No. 2.9e-84;
4; Mismatches 50;
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1.5e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 300;
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T25850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z19707 A; Accession: T23207
                                                                     A;Gene: CESP:T01B11.4
A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP
                                                                                                                                                                                                                                                                                       R;Geisel, C.; Stellyes, L. submitted to the EMBL Data Library, December A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T01B11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #teC;Accession: T25850
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A;Experimental source: clone K01H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K01H12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000 C;Accession: T23207
                                                                                                                                               A; Experimental source: C; Genetics:
                                                                                                                                                                  A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-313 <GEI>
                                                                                                                                                                                                                                                           A; Accession: T25850
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A; Residues: 1-313 <WIL>
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Best Local Similarity Matches 206; Conserv
                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAKDFLAGGVAAAISKTAVAFIBRVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKF
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                                                                         carrier protein; ADP, ATP carrier protein repeat
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                  66.5%; Score 1029; DB 2; 70.8%; Pred. No. 5.6e-84;
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; Pred. No. 5.6e-84;
28; Mismatches 53
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                                  Length 313;
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RESULT 14
A41677
ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
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A;Residues: 1-300 <LET>
A;Cross-references: RMBL:AF003141; NID:g2088732; PID:g2088738;
A;Cross-references: Strain Bristol N2; Clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Le, T.; Weinstock, L.; Rifkin, L. submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein W02D3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: T15206
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A; Accession: T15206
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                                                                                                                                                                                 TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
                                                                                                                                                                                                                        RAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRRMMMQSGRK-
                                                                                                                                                                                                                                            RAAYFGIYDTAKGML-PDPKNTHIVISMMIAQTVTAVAGLTSYPPDTVRRRMMQSGRKG
                                                                                                                                                                                                                                                                                                     LCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                          LCFVYPLDFARTRLAADVGKAGABREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS 127
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                                                                                                                                            -DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQ 297
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  #text_change 20-Aug-1999
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A; Status: preliminary
A; Molecule type: mRNA
A; Medlecule type: mRNA
A; Residues: 1-339 < HIL>
A; Residues: 1-339 < HIL>
A; Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
C; Superfamily: ADP, ATP carrier protein; ADP, ATP protein repeat homology carrier protein
C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F; 38-134/Domain: ADP, ATP carrier protein repeat homology carrier
F; 144-235/Domain: ADP, ATP carrier protein repeat homology carrier
F; 241-329/Domain: ADP, ATP carrier protein repeat homology carrier
                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-301 <ARS-
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A;Residues: 1-301 <ARS-
A;Residues: 1-301 <ARS-
A;Residues: 1-301 <ARS-
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat home
C;Keywords: duplication; transmembrane protein
F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hatin, I.; Jaureguiberry, G.
Eur. J. Blochem. 228, 86-91, 1995
A;Title: Molecular characterisation of the ADP/ATP-transporter cDNA
A;Reference number: S68993; MUID:95188918; PMID:7883016
A;Accession: S68993
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S51132
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R;Hilgarth; C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991

A;Title: Glucose increases the expression of the ATP/ADP translocator and A;Reference number: A41677; MUID:92084708; PMID:1748677

A;Accession: A41677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 GATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 MAFVKDILAGGTAGAISKTAVAPIERVKLILQTQDSNPMIKSGQVPRYTGIVNCFVRVSS
                                                                                                                             Ν
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                                                                                                      TDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITAD--KQYKGIIDCVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDBIKKF
                                                                                 SDIKTNFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIIYRAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQS
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                                                                                                                                                                                                     Score 938; DB 2; Pred. No. 6.8e-76;
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Pred. No. 1.7e-78;
9; Mismatches 64
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                                                                                                                                                                                                                              Length 301;
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8	63 RVSKEQGVLSLWRGNVANVIRYFFTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILS 121	FKDYFKNIF-PRYDONTDFSKFFCVNILS 1	121
¥	120 GGAAGATSICFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNV 179	EREPRGLGDCLVKIYKSDGIKGLYQGFNV 1	179
9	122 GATAGAISLLIVYPLDFARTRLASDIGK-GKORQFTGLFDCLAKIYKQTGLLSLYSGFGV 180	DRQFTGLFDCLAKIYKQTGLLSLYSGFGV 1	081
Ą	180 SVQGIIIYRAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRM 238	IVISWMIAQTVTAVAGLTSYPFDTVRRRM 2	238
8	181 SVTGIIVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPFDTVRRRM 240	IVLKWAVAQSVTILAGLISYPFDTVRRRM 2	240
Ą	239 MMQSGRKG-TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296	AFFKGAWSNVLRGMGGAFVLVLYDBIKK 29	8
8	241 MMSGRKGKEEIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELQK 299	GFFKGAWANVIRGAGGALVLVFYDELQK 29	99
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D12771; BAA02238.1; -.

    -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
    -!- SIMILARITY: Belongs to the mitochondrial carrier family.

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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKELETAL
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                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                 I PKEQEVLS FWRGNLANV I RYFPTQALNFA FKDKYKQI FLGGVDKRTQFWR YFAGNLASG
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                                                                                                                                                      I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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(POTENTIAL).
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; Murinae; Rattus
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G9 STRAID=2003 (Rel
D8 (Adenine nucleot
G9 STRAID=10090
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RN (2) TAXID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEXTULINE=20432087; PubMed=10974536; Levy S.E., Chen Y.-S., Graham B.H., "Expression and sequence analysis of translocase 1 and 2 genes."; Gene 254:57-66 (2000).
                                                                                                             EMBL; U27316; AAC52838.1; -.
EMBL; U10404; AAA19099.1; -.
EMBL; X70847; CAA51996.1; -.
EMBL; AF240003; AAF64471.1; -.
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01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
ADP,ATP carrier protein, fibroblast is
(Adenine nucleotide translocator 2) (A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis (1995), University
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLC25A5 OR ANT2.
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                                                                                                                                                                                                                                                                                                                                                       ween the SWIBS INSTITUTE. The European Bioinformatics Institutes as long by non-profit institutions as long by non-profit attement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
           MGI:1353496; Slc25a5
rPro; IPR002067; Mit_
rPro; IPR002030; Mit_1
                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een, the Swiss Institute of Bioinformatics and the EMBE outstation surpean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                              g requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                non-profit institutions and this statement is not requires a license agreement
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                                                                                                                                                                                                             v1-JUL-1993 (Rel. 26, Created)
VI 16-OCT-2001 (Rel. 40, Last sequence update)
ADP,ATP carrier protein, isoform T2 (ADP/ATP nucleotide translocator 3) (ANT 3)
SLC25A6 OR ANT3.
Bos taurne ''
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Best Local Similarity
                                       SEQUENCE FROM N.A.

MEDLINE-8929093; PubMed-2540808;

Powell S.J., Medd S.M., Runswick M.J., W.

"Two bovine genes for mitochondrial ADP/;

differences in various tissues.";

Biochemistry 28:866-873(1989).

-I- FUNCTION: CATALYZES THE EXCHANGE OF J.

MITOCHONDRIAL INNER MEMBRANE.

-I- SUBCELLULAR LOCATION: Integral membra
                                                                                                                                                                                                                                                             3 BOVIN
3 BOVIN STAN
ADT3 BOVIN STAN
P32007;
01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
16-OCT-2001 (Rel. 4
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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Multigene famil
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                                                                                                                                                                   NCBI_TaxID=9913;
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        DOMAIN: COMPOSED OF SIMILARITY: Belongs
                               inner membrane
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PR00784; MTUNCOUPLING.
PR00784; MITOCH CARRIER;
PR00215; MITOCH CARRIER;
PR00215; MITOCH CARRIER;
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98.0%;
         THREE HOMOLOGOUS DOMAINS to the mitochondrial cari
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Me.
                                          Integral membrane
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(ADP/ATP
                                                                                                            ADP/ATP
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                                                                                                    Walker J.s.;
P/ATP translocase
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                                          protein.
                                                                            AND
          carrier
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                                                                            ATP
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cora; Bovoidea;
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There are no restrictions og as its content is in

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Best Local
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MEDLINE=89236396; PubMed=2541251; Cozens A.L., Runswick M T
                                                                                                                                                                                                      ADT3_HUMAN STANDARD; PRT; 298 AA.
P12236; Q96C49;
01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, liver isoform T2 (AD (Adenine nucleotide translocator 3) (ANT 3).
                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             SLC25A6 OR ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCARRIER. PRINTS; PR00784; MIUNCOUPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling
InterPro; IPR001993; Mitoch_carrier
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up non-profit institutions as not 
modified and this statement is not removed. 
entities requires a license agreement (See
                                                                                                   NCBI_TaxID=9606;
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                  Walker J.E.;
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Pred. No. 7.7e
L3; Mismatches
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                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae
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.7e-121
                                                                                                                           Hominidae;
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GO; GO:0005744; C:mitochondrial inner membrane GO; GO:0005471; F:ATP/ADP antiporter activity; GO; GO:0006854; P:ATP/ADP exchange; TAS. InterPro; IPR002067; Mit_carrier. InterPro; IPR002030; Mit_uncoupling. InterPro; IPR001993; Mitoch_carrier.

translocase

60.

TAS.

EMBL; BC014775; AAH1 PIR; S03894; S03894.

AAH14775

HGNC:10992;

SLC25A6

EMBL;

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RX MEDILINE-22388257; PubMed=12477932;

RRA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RRA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RRA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RRA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RRA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RRA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RRA Hopkins R.F., Jordan K., Farmer A., Rubin G.M., Hong L.,

RRA Hopkins R.F., Jordan K., Farmer A., Rubin G.M., Hong L.,

RRA Hopkins R.F., Jordan R., Fonaldo M.F., Casavant T.L., Scheetz T.E.,

RRA Hopkins R.F., Jordan R., Fonaldo M.F., Casavant T.L., Scheetz T.E.,

RRA Hopkins R.F., Jordan R., Fonaldo M.F., Casavant T.L., Scheetz T.E.,

RRA Hopkins R.F., Jordan R., Fonaldo M.F., Casavant T.L., Scheetz R.J.,

RRA Hopkins R.F., Jordan R., Fonaldo M.F., Casavant T.L., Scheetz R.M.,

RICHARD S.S., McEwan P.J., McKernan K.J., Malak J.A., Gunaratune P.H.,

RRA Hopkins R.F., Jordan R., Fonaldo M.F., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Margolin
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Two distinct genes for ADP/ATP translocase are level in adult human liver.";
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          L; AV007135; AAA36750.1; -
L; AY007135; AAG01998.1; -
L; BC007295; AAH07850.1; -
L; BC008737; AAH08737.1; -
L; BC008935; AAH08935.1; -
L; BC008935; AAH08935.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eel in adult human liver.";
c. Natl. Acad. Sci. U.S.A. 85;377-381(1988).
c. NOTION: CATALYZES THE EXCHANGE OF ADP AND
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
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Biol. 206:261-280(1989)
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P48962; Q621
01-FEB-1996
                                                                                                     SEQUENCE FOR TISSUE-Brain;
STRAIN-C55EL/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
MEDLINE-97059403; PubMed-800724;
                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANC1).
SICC25A4 OR ANTI OR ANCI.
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                     Laplace C.
Submitted
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
SEQUENCE FROM N.A.
                                  STRAIN=BALB/c; TISSUE=Muscle;
Laplace C., Costet P.;
                                                        SEQUENCE
                                                                                       homologs."
                                                                                               Ellison J.W., Li X., Francke U., Shapiro I "Rapid evolution of human pseudoautosomal
                                                                                                                                         SEQUENCE FROM N.A.
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'S; PR00926; MITOCARRIER
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; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                          QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                                                                                                                                                                                                                                                          QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
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                                                     FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I PKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                      (SEP-1993)
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                                                                           7:25-30(1996).
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                     to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.7e-120;
3; Mismatches 9;
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                                                                                                                                                                          Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                          Murinae; Mus
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schepleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
REPEAT
CONFLICT
SEQUENCE
                                                                                                                                                      TRANSMEM TRANSMEM
                                                                                                                                                                                                              TRANSMEM TRANSMEM TRANSMEM
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TRANSMEM
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EMBL; X74510; CAA55616.1; -.
EMBL; AF240002; AAF64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC0026925; AAH26925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentives requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - ! - DOMAIN: COMPOSED OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S37210; S37210.
MGD; MGI:1353495; S1c25a4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932;
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translocase 1 and 2 genes.";
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"Expression and sequence analysis of the mouse adenine nucleotide
                                                                                             REPEAT
                                                                                                                                REPEAT
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      CRC64;
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Query Match

91.6%;

Score 1417;

DB 1;

Length 298,

Best Local Similarity

89.6%;

Pred. No.

3.1e-117;

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RESULT 7
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Q05962;
01-FEB-1994
InterPro; IPR002067; Mit carrier.
InterPro; IPR002030; Mit uncoupling.
InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X61667; CAA43842.1; -.
EMBL; D12770; BAA02237.1; -.
PIR; I60173; I60173.
                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP_ATP carrier protein, heart/skeletal muscle isoform ;
translocase 1) (Adenine nucleotide translocator 1) (ANT
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley, and Wistar; TISSUE-Heart, and MEDLINE=94002161; PubMed=8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Nammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLC25A4 OR ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLI
EXTENT, IN BRAIN AND KIDNEY.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch)
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MEDIJINE=8922903; FubMed=2540808;

Powell S.J., Medd S.M., Runswick M.J.,

"Two bovine genes for mitochondrial ADF
differences in various tissues.";

Biochemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase (Adenine nucleotide translocator 1) (ANT 1).
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                                                                                                           mitochondria.";
Hoppe-Seyler's Z. Physiol. Chem.
                                                                                                                                                     MEDLINE=82188267; PubMed=7076130;
Aquila H., Misra D., Eulitz M., Kling
"Complete amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                     MEDLINE=86295775; PubMed=3017341; Rasmussen U.B., Wohlrab H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
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  Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs
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InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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chem. Biophys. Res. Commun. 138:850-857(1986)
FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
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                                                                                                                                                                                                                                                                                                                                                                                                             PKEQGFLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGG
                                                                                                                                         SGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKF
                                                                                                                                                                                                                              QGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGLVSYPFDTVRRRWMQ
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RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang C.,

RA Brownstein M.J., Usdin T.S., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.S., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wagner G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

VIII Allon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

VIII Allon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

RE Proc. Matl. Acad. Sci. U.S. A. 99:16809-16003 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a reader peptide, divergence from a fibroblast translocator; and coevolution with mitochondrial DNA genes."; Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
[4]
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Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
"A human muscle adenine nucleotide translocator gene has four
"A human muscle adenine nucleotide translocator gene has four
is located on chromosome 4, and is differentially expressed.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last Sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle :
translocase 1) (Adenine nucleotide translocator
            Kaukonen J., Juselius J.K., Tiranti V., Kyttala A., Comi G.P., Keranen J., Peltonen L., Suomalainen A., "Role of adenine nucleotide translocator 1 in mtDNA Science 289:782-785(2000).
                                                                                                                                                                                 Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are
level in adult human liver.";
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Mammalia; Eutheria;
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K., Wade R.P., Shuster R., Wallace D.
a human skeletal muscle ADP/ATP trans
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Primates;
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nuclear genes
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Science 289:7

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GO; GO:00015207; F:adenine transporter activity; TAS.
GO; GO:0000002; P:entergy pathways; TAS.
GO; GO:0000002; P:mitochondrial genome maintenance; TAS.
GO; GO:0006832; P:small molecule transport; TAS.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR0012030; Mit_uncoupling.
InterPro; IPR0012030; Mit_uncoupling.
PRINTS; PR002030; Mitoch_carrier.
PRINTS; PR00204; MITOCARRIER.
PRINTS; PR00204; MITOCH_CARRIER.
PROSITE; PS00215; MITOCH_CARRIER.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest:
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
EMBL; BC008664; AAH08664.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   +
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SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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                                   I PKEQEVLS FWRGNLANVIRY FPTQALNFA FKDKYKQI FLGGVDKRTQFWRY FAGNLASG
1PKEQGFLSFWRGNLANV1RYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                     MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                         MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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V -> L (IN REF. 3).

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                    RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.B., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter S.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Bayayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Halsh M. Kalush P. Karpen G. H. K. Z. Kennison J.A. Ketchum K.A.
Fosler C., Ga
Glodek A., Go
Harris N.L.,
Hostin D., Ho
Jalali M., Ka
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"Molecular analysis of a candidate
isolation between sibling species of
Experientia 50:749-762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster shows a high degree ADP/ATP translocases.";
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase) (Adtranslocator) (ANT) (Stress sensitive B protein).
SESB OR A/A-T OR CG16944.
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Submitted (JAN-1997) to
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Zhang Y.Q., Davis
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MEDLINE=92389367; PubMed=1387687;
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Q26365; P91614; Q26254; Q95830; Q9VZ70;
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      Houston K. F., Kalush F.,
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A Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
A Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Melson D.R., Milshina N.V., Mobary L., Muzny D.M., Nelson D.L.,
A Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Palebo J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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A Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                            EMBL; $43651; AAB23114.1; -.

EMBL; $71762; AAB31734.3; -.

EMBL; $71762; AAB31734.3; -.

EMBL; $10618; CAA71528.1; -.

EMBL; AE003484; AAF47957.1; -.

EMBL; AV070894; AAL28526.1; -.

EMBL; AV070894; AAL28526.1; -.

EMBL; AV070894; AAL28526.1; -.

EMBL; AV070894; AAL28526.1; -.

EMBL; AV070894; C:mitochondrial inner membrane; IE

GO; GO:0006743; C:mitochondrial transport; IMP.

InterPro; IPR001993; Mit carrier.

InterPro; IPR001993; Mitoch carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley; TISSUB-Larva, Ovary, and Pupae; MEDLINE=22426066; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu C., George R.A., Guarin H., Kronmiller B., Pacleb J., Rubin G.M., Celniker S.E.; "A Drosophila full-length cDNA resource.", Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (200-1-FUNCTION: Catalyzes the exchange of ADP and mitochondrial inner membrane.
                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito carr; 2. PRINTS; PR00926; MITOCARRIER. PROSITE; PS00215; MITOCH_CARR
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SUBCELLULAR LOCATION: Integral membrane
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10 -> A (IN REF. 2)
11 -> S (IN REF. 1)
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5 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ini
Neoptera; Endopterygota; Diptera; Nematocera.
NCBI TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last amotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
                                    PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRI
Mitochondrion; Inner membrane;
                                                                                                                                                                                                                                                                                                                                      Insect Mol. Biol. 3:35-40 (1994).
-- FUNCTION: CATALYZES THE EXCHANGE O
-- MITOCHONDRIAL INNER MEMBRANE.
-- I- SUBUNIT: Homodimer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                              "A cDNA encoding an ADP/ATP carrier from gambiae.";
                                                                              InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
Pfam; PP00153; mito_carr; 3.
                                                                                                                        EMBL; L11618; AAB04104.1;
EMBL; L11617; AAB04105.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94348635; PubMed=8069414; Beard C.B., Crews-Oyen A.E., Kuma
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                                                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                            inner membrane
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Pred. No. 7.1e-103;
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C P31592;

T 01-UTL-1993 (Rel. 26, Created)

T 01-UTL-1993 (Rel. 26, Last sequence update)

JT 01-UTL-1993 (Rel. 36, Last annotation update)

DE ADP, ATP carrier protein (ADP/ATP translocase) (Av translocator) (ANT).

OS Chlorella kessleri.

OC Bukaryota, Viridiplantae; Chlorophyta; Trebouxic
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Best Local S
Matches 227
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Hilgarth C., Sauer N., Tanner W.;
"Glucose increases the expression of the ATP/ADP translocator and glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
J. Biol. Chem. 266:24044-24047(1991).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-i- SUBCULTILAR LOCATION: Integral membrane protein. Mitochondrial
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                              PIR; A41677; A41677.
InterPro; IPR002067; Mit carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                EMBL; M76669; AAA33027.1;
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TRANSMEM 248
TRANSMEM 304
SEQUENCE 339
                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                               STRAIN-cv. Texas Marker 1; TISSUE-Fiber;
Shin H., Brown R.M. Jr.;
"Two cDNA sequences for the adenine nucleotide translocator, CANTI
CANT2, from cotton fibers (Gossypium hirsutum).";
(In) Plant Gene Register PGR97-130.
-1- SUBCELLULAR LOCATION; Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum (Upland cotton).

Gossypium hirsutum (Upland cotton).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidi
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                       022342;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-FBB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein 1, mitochondrial precursor
translocase 1) (Adenine nucleotide translocator 1)
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                                                    EMBL; AF006489; AAB72047.1;
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                                                                                                                                                                                                                                                                                                                                                                                              ANT1.
                                                                                                                                                                                       inner membrane (By similarity).
SIMILARITY: Belongs to the mitochondrial carrier family.
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2 (POTENTIAL).
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54779734A33B3942 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386
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.9e-78;
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MBL outstation -
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T09709;

InterPro; IPR002067; Mit_carrier. InterPro; IPR001993; Mitoch_carri

mito_carr;

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Best Local
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ANCI OR SPBC530.10C.
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                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., I Sgouros J., Peat N., Hayles J., Baker S.
                                                                                                                               Saccharomyces cerevisiae.";
Gene 171:113-117(1996).
                                                                                                                                                                  Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.; "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation
                                                                                                                                                                                                                                    MEDLINE=96257204;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
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                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       PubMed=8675018;
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Pred. No. 2.3e
35; Mismatches
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No. 2.
  Lyne M., L
S., Basham
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:3e-60;
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  Lyne
m D.,
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                        Stewart
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RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Vonstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Woodward J., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Woodward J., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002)
C. — ITONCTIONNER MEMBRANES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion;
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    -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
    -!- SIMILARITY: Belongs to the mitochondrial carrier family.

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InterPro; IPR001993; Mitoch_carrier.
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DOMAIN: COMPOSED OF
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                                                                                                                                                                                                                                                                                                                                  Similarity
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; PS00215; MITOCH_CARRIER; 2.
     GATSLCFVYPLDFARTRLAADV--GKAGAERBERGLGDCLVKIYKSDGIKGLYQGFNVSV
                                                                                                                                                                                                                          SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADK---QYKGIIDCVVRIPK
                                                                       EEGVISLWRGNTANVLRYPPTQALNFAFKDKFKKMF
                                                                                                        TFFFDFMMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIRAGRLSHRYKGIGECFKRTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                   MW.
                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                 Pred. No. 2.3
                                                                                                                                                                                                                                                                                                                               Score 770;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                             2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 AC3D16A40F41AFC CRC64;
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les 74;
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                                                                                                                                                                                                                                                                                                    Gaps
              181
                                                                       142
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GAASILFVYSLDYARTRLANDAKSAKKGGERQFNGLVDVYRKTYRSDGLRGLYRGFGPSV

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                                                                                                                Query Match
Best Local 9
                                                                                           Matches
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01-AUG-1992
01-AUG-1992
                                                                                                                                                                                  TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sharpe J.A., Day A.;
"Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";
Mol. Gen. Genet. 237:134-144(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                      TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                  TRANSMEM TRANSMEM
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01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X65194; CAA46311.1; -.
PIR; S30259; S30259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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nterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLRE
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    PS00215; MITOCH_CARRIER; 2.
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                                                                                                                                                                                    308 AA;
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                               Inner
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92
133
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29 1
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Pred. No. 6e-60;
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1 (POTENTIAL).
2 (POTENTIAL).
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                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                         (POTENTIAL).
                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                               Transmembrane;
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                                                                                                                                                                         126 TSLCFVYPLDFARTRLAAD---VGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQ
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                                                    S---
                                                                                                                                                                                                            GFGSLWRGNTANVIRYFFTQALNFAFKDKFKRWF--GFUKDKEYWKWFAGUMASGGAAGA
                                                                                                      GIVVYRGLYFGMYDSLKPVVLVGPLANNFLAAFLLGWGITIGAGLASYPIDTIRRRMMMT
                                                                                                                            GIIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQ 241
KY 303
                       KY 297
                                                                           SGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEI-----K
                                                                                                                                                         VSLSFVYSLDYARTRLANDAKSAKKGGGDRQFNGLVDVYRKTIASDGIAGLYRGFNISCV
                                                   -GSAVKYNSSFHCFQEIVKNEGMKSLFKGAGANILRAVAGAGVLAGYDQLQVILLGK
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Search completed: December 18, 2003, 12:41:24
Job time: 9.34267 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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seq length: 2000000000
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, <u>ب</u>. derived by analysis of the total score distribution

SUMMARIES

44440000	Result No.
1543 1543 1543 1543 1543 1463 1463 1454	Score
100.0 100.0 100.0 100.0 100.0 94.2 94.2	Query Match
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AAY71033 AAM39641 AAU10200 AAU10380 AAW41427 AA018516 AAY71032 AAU101199 AAU10379	IJ
Human adenine nucl Human polypeptide Human adenine nucl Human adenine nucl Human insulin recee Human adenine nucl Human adenine nucl Human adenine nucl	Description

	AAG38670	21	1027	48.1	742.5	45
	AAG38671	21	1009	48.1	742.5	44
	AAG38672	21	992	48.1	•	43
	AAG38458	21	381	48.1		42
	AAG37262	21	381	48.1	742.5	41
	AAG37259	21	381	48.1	742.5	40
	AAG36575	21	381	48.1	742.5	39
	AAG38459	21	363			38
	AAG37263	21	363	•	742.5	37
thali	AAG37260	21	363		742.5	36
	AAG36576	21	363	48.1	742.5	35
	AAG38460	21	346	48.1	742.5	34
thali	AAG37264	21	346	48.1	742.5	33
	AAG37261	21	346	48.1	742.5	32
	AAG36577	21	346	48.1	742.5	31
Arabidopsis thalia	ABP81267	24	379	48.2	743	30
ADP/ATP carrier pr	AAM00106	22	386	48.6	749.5	29
	ABG27055	22	484	49.4	763	28
Novel human diagno	ABG15422	22	484	49.4	763	27
o.	ABP73357	23	301	51.1	788.5	26
human diag	ABG18922	22	298	57.0	879.5	25
	ABP74106	23	222	63.6	981	24
ovarian a	ABP43205	23	228	67.7	1044	23
Human TRICH-19 pro	AAB21175	23	315	72.5	1119	22
Human metabolism-a	ABU53218	22	315	72.5	1119	21
Drosophila melanog	ABB58380	22	307	73.7	1137.5	20
Drosophila melanog	ABB67300	22	299	81.3	1254.5	19
Ō	ABB66082	22	299	81.3	1254.5	18
	ABG27056	22	263	83.5	1288	17
	ABG15423	22	325	88.6	1367.5	16
	AAU10378	23	297	89.8	1385.5	15
adenine nuc	AAU01198	22	297	89.8	1385.5	14
adenine nuc	AAY71031	21	297	٠	1385.5	13
n metabolis	ABU53219	22	293		1406	12
proteir	AAW61169	19	298	91.5	1412	11
Human DITHP organe	ABR41715	24	429	91.9	1418	10

ALIGNMENTS

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Human adenine nucleotide translocator ANT3.
                                     29-AUG-2000
                                                                          AAY71033;
                                                                                                              AAY71033 standard; Protein; 298
                                   (first entry)
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PR 03-N
PR 08-S Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nottropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leer's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy, lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

WO200026370-A2

03-NOV-1999; 11-MAY-2000 99WO-US25883

03-NOV-1998; 08-SEP-1999; 98US-0185904. 99US-0393441.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Ghosh SS;
peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                  Human polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM39641 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365619/31.
N-PSDB; AAD00521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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llarity 100.0%;
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Pred. No. 4.6e-157;
; Mismatches 0;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                       in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Include the utilisation of the activities such as Inmune system suppression, Activinjinhibin activity, chemotactic/chemokinetic activity, hamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
Wang
Zhao
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                  C.N.S disorders.
Note: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 2786; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-)
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DB; AAI58797.
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Wang Z,
Zhou P,
                 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                      GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                          IPKEQGVLSFWRGNLANVIRYPPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                              MTEQAISFAKDFLAGGIAAAISKTAVAFIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                    GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                         I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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RESULT 3
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                                                                                                                                                                                                                                                                                                                    The present sequence represents human adenine nucleotide translocator-3

(ANT-3) protein. ANT proteins are mitochondrial permeability

transition (MTP) pore components responsible for mediating transport

of ADP across the mitochondrial inner membrane. ANT proteins interact

with other mitochondrial core components e.g. cyclophilins to

regulate MPT. The present invention relates to a novel nucleic acid

expression construct comprising a promoter operably linked to a

polynucleotide encoding a mitochondrial pore component polypeptide

(e.g. ANT) fused to an energy transfer molecule (ETM) protein

(c.g. green fluorescent protein (GFP) or a FLASH sequence). The novel

expression construct can alter mitochondrial membrane permeability

transition and/or alter the interaction between mitochondrial core

components. The methods are useful for screening for agents that alter

treatment of diseases associated with altered mitochondrial function or

dysfunctional cell survival, such as Alzheimer's disease, diabetes

mellitus, Parkinson's disease, Huntington's disease, schizophrenia,

mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                             Query Match
Best Local Similarity
Matches 298; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                   hyperproliferative
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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larity 100.0%;
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                                                                                                       <u>,</u>
                                                                                                 Score 1543; DB 22;
Pred. No. 4.6e-157;
; Mismatches 0;
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RESULT 4
AAU10380
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cc encoding an adenine nucleotide translocator (ANT) polypeptide. ANT crosses and adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial cc matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and cc culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is cc expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT cuseful for determining the presence of an ANT polypeptide. CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating covalently bound to a solid phase. Detectably labeled ANT ligand is covalently or non-cc covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
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Ghosh SS,
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUG-2000;
14-SEP-2000;
                                                                                                                                            Tang
Wang
Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                           Zhao
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                                                            N-PSDB;
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.N.
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                                                                                                                                                                                                                                                                                                                                                                                                              Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA018516;
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                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                             n; insulin receptor signaling; insulin receptor signaling diabetes; metabolic syndrome; antidiabetic.
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                                                                                                                                                                  2002WO-US01048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor signaling modifier
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Pred. No. 5.2e-157;
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                                                                                                                                                                                                                                                                                                                                                                                                                 modifier;
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                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.
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12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an insulin receptor signaling modulator, useful as ditargets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 160-161; 232pp;
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DB; AAL48635.
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               QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                       VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                       I PKEQGVLS FWRGNLANVIRYF FTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
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2001US-261531P.

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Pred. No. 1.8e-:
13; Mismatches
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1.8e-148;
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                                                                                                       inner mitochondrial membrane. It mediates transport of adenosine at an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial incurbanty, schizophrenia, mitochondrial diabetes and stroke (MELNS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANTZ from human brain.
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Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic against mitochondrial disease
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 45; Page 172-173; 175pp; English
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N-PSDB; AAD00520.
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/ Match 94.2%;
Local Similarity 92.6%;
les 274; Conservative
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99US-0393441.
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Score 1454; DB 21;
Pred. No. 1.7e-147;
3; Mismatches 9;
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transition (MTP) pore components responsible for mediating transport of ADP across the micochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter treatment of disease associated with altered mitochondrial function or treatment of disease associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murphy AN, C. Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial
mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenine nucleotide translocator-2 (ANT-2) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents human adenine nucleotide translocator-2
P-2) protein. ANT proteins are mitochondrial permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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3, Davis RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           permeability transition pore component; cell survival;
core component; mitochondrial related disorder; cancer;
isease; diabetes mellitus; hyperproliferative disorder.
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Best Local (
                                                                                                                                                        Anderson C
Ghosh SS,
                                                                                                                             WPI; 2002-055598/07
N-PSDB; AAS16689.
                                                                                                                                                                                                                                                                                               Human; adenine nucleotide translocator; ANT; 88; mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorders e.g. cancer,
                                                                                                                                                                                                      11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                       11-MAY-2001; 2001WO-US15416
                                                                                                                                                                                                                                           15-NOV-2001
                                                                                                                                                                                                                                                            WO200185944-A2
                                                                                                                                                                                                                                                                                                                           Human adenine nucleotide translocator 2 (ANT2).
                                                                                                                                                                                                                                                                                                                                              14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                       OSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
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Pred. No. 1.7e
3; Mismatches
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1.7e-147;
                                                                                                                                                                  Wiley SE,
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comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell culturing the host cell. (I) is also useful for targeting a polypeptide

for targeting a polypeptide

and

The invention relates to a recombinant expression construct

Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide

for producing adenine nucleotide regulated promoter linked to

Claim 44; Fig 2; 147pp;

English.

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RESULT 10
ABR41715
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28-MAR-2001;
29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide, antigand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                                                                                                                                         cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
                                                                                                                                           27-MAR-2002;
                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                   organelle-associated
                                                                                                                                                                                                                                                                                gene therapy; antisense therapy; genot disease model; toxicological testing;
                                                                                                                                                                                                                                                                                                                                                            Human; dithp; diagnostic and therapeutic polymucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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 2001US-279619P.
2001US-2800667P.
2001US-280068P.
2001US-291280P.
2001US-291280P.
2001US-291829P.
2001US-299428P.
2001US-299476P.
                                                                                                                                                                                                                                                                                                                                                                                                         organelle-associated protein
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Pred. No. 1.7e-147;
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Daughtery SC, L. David M
Peralta CH, David M
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David MH,
Marwaha R,
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Liu TF, Nguyen DA,
Lewis SA, Chen AJ,
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Urashka MB;
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Harris B;
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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies -

SEQ ID No 1250; 591pp; English.

CC polymucleotides designated dithp (ACC46080-ACC46749) and to their CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates CC to polymucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and CC transgenic organisms comprising adithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP CC proteins; microarrays comprising dithp nucleic acid sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of sessessing the toxicity of test compounds using a dithp hybridisation comprise of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, curial, fungal or parasitic infections; hormonal disorders; metabolic compounds can additionally be used in analysis of the proteins can additionally be used in analysis of the proteins can additionally be used in analysis of the proteome of a tissue correct type and to induce antibodies. The dith nucleic acids are corrected animals, in toxicological testing, and in transcript imaging. The present sequence represents a DITHP protein which is an organelle-corrected mentioned animals, in toxicological testing, and in transcript imaging. The present sequence represents a DITHP protein which is an organelle-casted mythers. The invention relates to novel human diagnostic and therapeutic molvnucleotides designated dithp (ACC46080-ACC46749) and to the Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly associated protein. ftp.wipo.int/pub/published_pct_sequences. of the printed

Sequence 429 B

Similarity

91.9%; 95.2%;

Score 1418; DB 2 Pred. No. 2e-143;

24;

Length

429;

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Best Local S
Matches 277
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                                                                   GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                      I PKEQGVLS FWRGNLANVI RYF FTQALNFAFKD KYKQI FLGGVD KHTQFWRYFAGNLASG
                                                                                                                                                          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                    GAAGATSLCFVYPLDFARTRLAADVGKSGTERE
                                                                                                        1PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQ1FLGGVDKHTQFWRYFAGNLASG
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AAW61169
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                                                                                                                               Matches
                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                         The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into APP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ant1; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 39-40; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-286608/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graham BC, Macgregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996;
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                                                                                                                                                                                                                              independent of ANT1.
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 61
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                                                                                                                                                Similarity
                    I PKEQGVLS FWRGNLANV I RY F PTQALNFA FKDKYKQ I FLGGVDKHTQFWR Y FAGNLASG
 I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDRHKQFWRYFAGNLASG
                                                                  MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                   MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                               Conservative
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                                                                                                                                              91.5%;
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                                                                                                                                              Score 1412; DB 19;
Pred. No. 5.4e-143;
                                                                                                                               Mismatches
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                                                                                                                                                               Length
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                                                                                                                               Gaps
                                  120
 120
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QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124

120

AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE

ALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE

60

Query Match Best Local S Matches 263

al Similarity 263; Conserv

Conservative

91.1%; 17;

Score 1406; DB 22; Pred. No. 2.3e-142; L7; Mismatches 12;

Indels Length

Gaps

293; <u>;</u>

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RESULT 12
ABU53219
ID ABU53219
ID ABU53
XX ABU53
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                                                                 This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies -
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example III; Page 850; 1095pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wiemann
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28-SEP-1999;
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       293 AA;
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(ANY) proteins or ANY is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANY is used to identify agents or ligands that bind to, or interact with it. The ANY ligands are used to detect or isolate ANY in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MTT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 44; Page 172; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant construct encoding adenine nucleotide translocator , polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1998;
08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                        patent discloses a method to produce adenine nucleotide translocator
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DB; AAD00519.
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99US-0393441
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                           Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT1 from human brain.
                                                          New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                          Murphy AN, Ci
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                              mitochondrial
mitochondrial
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                                                                                                                                                                                                                                                                                                   WO200132876-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenine nucleotide translocator-1 (ANT-1) protein
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                                                                                                                                                                                                  (MITO-) MITOKOR.
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DB; AAS05901.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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                                                                                                                                                             Clevenger W,
3, Davis RE;
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                                                                                                                                                                                                                                                                                                                                                 permeability transition pore component; cell
core component; mitochondrial related disord
isease; diabetes mellitus; hyperproliferative
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Pred. No. 3.8e-140;
1; Mismatches 16;
                                                                                                                                                                         SB,
                                                                                                                                                                         Andreyev
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The present sequence represents human adenine nucleotide translocator-1 (ANT-1) protein. ANT proteins are mitochondrial permeability

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English

of ADP across the mitochondrial inner membrane. ANT proteins interac

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention of treatment of diseases associated with altered mitochondrial function dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GPP) or a FLASH sequence). The nove
                   Anderson CM, Davis RE, Clevenger W, W Ghosh SS, Moos WH, Pei Y, Carroll AK;
                                                                                                   11-MAY-2000; 2000US-0569327
                                                                                                                                  11-MAY-2001; 2001WO-US15416
                                                                                                                                                                                                      WO200185944-A2
                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                     Human; adenine nucleotide translocator; mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                     Human adenine nucleotide translocator 1 (ANT1).
                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10378 standard;
                                                                   (MITO-) MITOKOR.
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                                  Miller SW,
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CC comprising a regulated promoter operably linked to a nucleic acid comprising an adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC culturing the host cell. (I) is also useful for targeting a polypeptide of culturing the host cell.) is also useful for targeting a polypeptide is CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide of interest.) (CC expressed as a fusion protein with the polypeptide of interest.) (CC expressed as a fusion protein with the polypeptide of an ANT polypeptide.) (CC expressed as a fusion agent that binds to an ANT polypeptide.) (CC expressed is useful for ANT3 in a biological sample and for isolating CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC expressed as a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. (CC expressed and contently bound to a solid phase between the antipolation of human ANT1. (CC expressed and contently bound to a solid phase and contently bound to a solid phase of the present sequence of human ANT1.
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid
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                                                                                         297 AA;
89.8%;
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                            DB 23;
                            Length
                               297;
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á Ś 밁 Ś 밁 밁 S 밁 S Query Match Best Local S Matches 260 241 240 180 181 121 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180 61 61 260; Н 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKKVI 298 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM Conservative 21; Score 1385.5; DB 2 Pred. No. 3.8e-140; 11; Mismatches 16; 16; Indels 1; Gaps 240 120 120 60

Similarity

December 18, 2003, 12:40:47

Job time : 36.3729

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Result
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US-08-9434-354-48
US-08-941-871-10
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US-09-18-158-2
US-09-160-119-4
US-09-160-119-2
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US-08-470-861A-51
US-08-470-861A-51
US-08-470-861A-51
US-08-947-983-51
US-08-947-983-51
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205.5	205.5	205.5	205.5	211	222	226.5	226.5	226.5	226.5	226.5	226.5	227.5	232.5	232.5	243.5	244	244
13.3	13.3	13.3	13.3	13.7	14.4	14.7	14.7	14.7	14.7	14.7	14.7	14.7	15.1	15.1	15.8	15.8	15.8
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Sequence 56, Appl	Sequence 56, Appl	Sequence 56, Appl	Sequence 56, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	Sequence 36, Appl	•	Sequence 12, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli

ALIGNMENTS

CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-49 8 片 S ₽ Ş 맑 ঠ 밁 US-09-434-354-49 APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E. Sequence 49, Application Patent No. 6562563 GENERAL INFORMATION: Query Match 100.0%; Score 1543; DB 4; Best Local Similarity 100.0%; Pred. No. 4.5e-166; Matches 298; Conservative 0; Mismatches 0; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITCCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433 241 181 181 121 241 121 13 13 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120 **OSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI** VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM US/09434354 0; Length 298; Indels 0, Gaps 180 180 240 60 0

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US-09-434-354-48
                                                                                                                                                                                                                                      Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Graham, Grant R.
APPLICANT: MacGregor, Grant R.
APPLICANT: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10,
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Holdryev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
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TYPE: PRT
ORGANISM: Homo sapien
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                              NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                              CITY: Boulder STATE: Colora
                                                                    ZIP: 80303
                                                                                        COUNTRY:
                                                                                                                                                      STREET:
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                                                                                                              Colorado
                                                                                                                                                      ?E: Greenlee, Winner and Sullivan, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                           Application US/08961871
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FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297

ORGANISM: Homo sapien

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                                                                                                                                                                                                                                                                      Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 264; Conservative
                                                                                                                                                                                                                                                   Patent No.
APPLICANT: Murphy, Anne N.
APPLICANT: Mily, Anne N.
APPLICANT: Mily, Sandra Eileen
APPLICANT: Mily, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEPAX: (303) 499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
PILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DUS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/961,871
FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                   47, Application US/09434354
o. 6562563
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                                                                                                                                                                                                                                                                                                                                                                                    QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
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; Pred. No. 2.9e-151;
19; Mismatches 15;
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C13
CCURRENT APPLICATION NUMBER: US/09/996,243
CCURRENT PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PRILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
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Matches 260
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DR APPLICATION NUMBER: 60/065311

DR FILING DATE: 1997-11-13

DR APPLICATION NUMBER: 60/066770

DR FILING DATE: 1997-11-24

DR APPLICATION NUMBER: 60/075945

DR FILING DATE: 1998-02-25
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o. 6478825
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Baker, Kevin P.
Botstein, David
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Williams, P. Mickey
Wood, William I.
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Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                       Paoni, Nicholas F.
Roy, Margaret Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                    Napier, Mary A.
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                                                                                                                                                                                                                                                                                                                           Timothy A.
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87.2%; Pred. No. 2.9e
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APPLICATION NUMBER: 60/089599

APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-1

FILING DATE: 1998-06-17

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1998-06-17

PILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252

APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908

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1998-06-19

APPLICATION NUMBER: 60/089947

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APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/089653

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SOFTWARE: FastSEQ for
SEQ ID NO 339
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Best Local Similarity
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Patent No. 61505
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
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Pred. No. 1.7e-26;
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Pred. No. 7.8e-27;
0; Mismatches 115;
                                                                                                                                                                                                                     Length 469
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APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690

FILING DATE: 1998-06-25

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676

LING DATE: 1998-06-25

APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090542

FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472

1998-06-24

FILING DATE:

APPLICATION NUMBER: 60/090435

APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24

FILING DATE:

1998-06-24

APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090444

LING DATE:

1998-06-24

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/090429

1998-06-23

1998-06-24

FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090254

FILING DATE: 1998-06-22 FILING DATE: 1998-06-:

APPLICATION NUMBER: 60/090355

APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091478 APPLICATION NUMBER: 60/091360

NUMBER: 60/091519 1998-07-01 FILING DATE: 1998-00 APPLICATION NUMBER:

LING DATE:

FILING DATE:

1998-07-01 1998-06-26 APPLICATION NUMBER: 60/090862

1998-06-26

60/090863

FILING DATE: 1998-06-25

APPLICATION NUMBER: 60/090696

LING DATE:

1998-06-25

APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25

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US-09-312-283C-339
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                GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OP INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
                                                                                                                                                                                               Sequence 118, Application US/09482273 Patent No. 6534631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ORGANISM: Mouse
-09-312-283C-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/312,283C CURRENT FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Watson, James APPLICANT: Strachan, Lor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                                                                         405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 IDLAVÝETL-----KNTWLQRYAVNSADPGVFVLLACGTISSTCGQLASÝPLALVRTR 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASR----SNNMCIVGGFTQMIREGGAKS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339, Application
o. 6573095
  APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAKEGVAAFYKGYIPNMLGIIPYAG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWRGNGINVLKIAPESAIKFMAYEQMKR--LVGSDQET---LRIHERLVAGSLAGAIAQS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDELK 295
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                                                                                                                                                                                                                                                                                                                                    MQAQASIEGAPEVTMSSL--PKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK 461
                                                                                                                                                                                                                                                                                                                                                                                                                           IDLAVYETL-----KNTWLQRYAVNSADPGVFVLLACGTISSTCGQLASYPLALVRTR 404
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Sleeman, Matthew
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NUMBER: 60/092,921
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Pred. No. 1.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 111; Indels
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (335)
; OTHER INFORMATION: Xaa (US-09-482-273-118
                                                                                                                                                                                                        ; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2
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US-09-501-558-2
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Best Local Similarity
Matches 87; Conserv
                                                                                                                       Query Match 18.4%; Score 283.5; DB Best Local Similarity 28.9%; Pred. No. 1.1e-23 Matches 87; Conservative 54; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander
APPLICANT: Mathur, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09501558 Patent No. 6403784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins
TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins
TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins
TITLE OF INVENTION: NO. 6403784el Human Uncoupling Proteins
TITLE OF INVENTION: Polymolectics
TITLE OF INVENTION: 000-012-09
NUMBER OF SEQ ID NOS: 4
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                                                             KDFLAGGIAAAISKTAVAPIERVKLLLQVQHAS-----KQIAADKQYKGIVDCIVRIPKE
QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124
                                       KPFVYGGLASITAECGTFPIDLTKTRLQIQGQTNDAKFKEI----RYRGMLHALVRIGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIVVGVELPVYDITKKHLILSGMMGDTILTHFVSSF----TCGLAGALASNPVDVVRTRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VISSTIANPTDVLKIRMQA----QGSLFQGSMIGS-FIDIYQQEGTRGLWRGVVPTAQRA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGVLALYSGIAPALLROASYGTIKIGIYQSLKRLFVERLEDET-----LLINMICGVVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPFVYGGLASIVABFGTFPVDLTKTRLQVQGQSIDARFKEI----KYRGMFHALFRICKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOFLAGGIAAAISKTAVAPIERVKLLLQVQHAS----KQIAADKQYKGIVDCIVRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zambrowicz, Brian
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                                                                                                                                                                                                                                                                                                                  for Windows Version 3.0
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; Pred. No. 6.9e-24;
50; Mismatches 133;
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                                                                                                                       Indels 31;
                                                                                                                                                              Length 291;
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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US-09-160-119-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 447
TYPE: PRT
ORGANISM: HOMO SAPIENS
S-09-160-119-4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: EP 98401655.0 EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: GH-30985
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                              GCAGGSQVIFTNPLEIVKIRLQV-AGEITTGPRVSAL----SVVRDLGFFGIYKGAKAC
                                                                                                                                                                                                                                                                                                                                                         QVAESÁYRFGLGSVÁGÁVGATÁVYFÍDLVKTRMÓNÓRSTGSFVGELMÝKNSFDCFKKVLR
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ilarity 27.1%;
Conservative 4
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pred. No. 5.1e-23;
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    Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/142,565A.
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
RUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-142-565-2
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                                                                       SEQ ID NO 2
LENGTH: 312
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SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
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Best Local Similarity
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APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
ORGANISM: HOMO SAPIEN
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Kelly Paine
APPLICANT: ROBERT James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
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FILE REPERENCE: GH-30985
CURRENT EPPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                 LENGTH: 31
TYPE: PRT
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ORGANISM: HOMO SAPIENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKCAWSNVLRGMGGAFVLVLYDEL
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546

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17.2**%;** 27.1**%**;

Score 265; DB 3; Pred. No. 1.5e-21;

Length 312;

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US-08-518-878B-56
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                                     Matches
                                                                    Query Match
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                                                                                                                                                                                            TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/518,878B
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 785:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                            TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                           PILING DATE: 23-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION:
                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                           LENGTH:
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12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELK 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL-GGVDKHTQFWRYFAGNLASGGAA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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                                                                                                                                                                         299 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tartaglia, Louis A.
VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS,
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                                                                                                                          unknown
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                                                                                                                                           single
                                                    16.2%; Score 250.5;
24.9%; Pred. No. 6e
                               52;
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                                                                                                                                                                                                                                                                                                        7853-036
                                 Mismatches 146;
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                                                      6e-20;
                                                                   DB 1;
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                                   Indels
                                                                   Length 299;
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                                 25;
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                                                                                                                                                                     Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                             TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CONIZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tartaglia, Louis C. TITLE OF INVENTION: Compositic TITLE OF INVENTION: Treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                     LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
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                                    69 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
                                                                                                               12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
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SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 121
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                                                                                                                                                       Conservative
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                                                                                                                                                                     16.2%;
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                                                                                                                                                   Score 250.5; DB
Pred. No. 6e-20;
52; Mismatches 1
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US-08-518-878B-51
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INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   Query Match
'Best Local Similarity
Matches 74; Conserv
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GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 57
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191 CABLVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM--- 243
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                                             189 AAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQS 242
                                                                                       132 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 190
                                                                                                                 129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIXR 188
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1155 Avenue of the Americas
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NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 298		GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
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Search completed: December 18, 2003, 12:44:56 Job time : 13.3471 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

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1543
1 MTEQAISFAKDFLAGGIAAA......LRGMGGAFVLVLYDELKKVI 298
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	14	13	12	11	10	9	8	7	6	ហ	4	ω	N	_	No.	Result	
737	737	749.5	760.5	788.5	811	1385.5	1385.5	1385.5	1454	1454	1454	1543	1543	1543	Score		
47.8	47.8	48.6	49.3	51.1	52.6	89.8	89.8	89.8	94.2	94.2	94.2	100.0	100.0	100.0	Match	Query	æ
308	308	386	318	301	179	297	297	297	298	298	298	298	298	298	Match Length DB		
15	15	9	10	12	12	10	9	9	10	9	9	10	9	9	8		
US-10-128-714-8338	US-10-128-714-3338	US-09-734-569-170	US-09-801-368-252	US-10-032-585-7194	US-10-029-386-32501	US-09-185-904A-31	US-09-810-644-31	US-09-811-094-31	US-09-185-904A-32	US-09-810-644-32	US-09-811-094-32) US-09-185-904A-33	US-09-810-644-33	US-09-811-094-33	ID	•	
Sequence 8338, Ap	Sequence 3338, Ap	Sequence 170, App	Sequence 252, App	Sequence 7194, Ap	Sequence 32501, A	Sequence 31, Appl	Sequence 31, Appl	Sequence 31, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 33, Appl		Description		

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	314	326	333.5	368	368	423	518	686	
20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	21.1	نر	23.8	w	27.4	33.6	44.5	
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US-09-997-653-289	US-09-989-734-289	US-09-993-687-289	US-09-990-436-289	US-09-989-730-289	US-09-991-181-289	US-09-990-444-289	US-09-989-735-289	US-09-989-293A-289	US-09-992-598-289	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	US-09-989-732-289	US-09-989-731-289	US-09-989-727-289	US-09-989-279-289	US-09-989-723-289	US-09-989-722-289	US-10-094-749-1789	US-09-777-921A-5	US-09-777-921A-2	US-09-777-921A-4	US-09-864-761-36440	US-09-925-301-1459	US-10-259-165-192	
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ALIGNMENTS

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RESULT 2
US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
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  Sequence 33, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
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APPLICANT: Davis, Robert B.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
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LENGTH: 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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Local Similarity 100.0%;
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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Anderson, Christ
Davis, Robert E.
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Pred. No. 1e-156;
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088,420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANI

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/105,904A

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 33

LENGTH: 298

TUTE OF INVENTION OF ADENINE NUMBER OF SEQ ID NOS: 33

LENGTH: 298
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; ORGANISM: Homo US-09-811-094-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/09811094 Patent No. US20010044144A1 GENERAL INFORMATION:
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Matches 298; Conserv
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Best Local
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Davis, Ro
APPLICANT: Clevenger
                                          TYPE: PRT
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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                 sapien
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Pred. No. 1e-156;
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Query Match Best Local Similarity

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Score 1454; DB 9; Pred. No. 3.5e-147;

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US-09-810-644-32
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APPLICANT: Davis, Robert E
APPLICANT: Clevenger, Will
APPLICANT: Wiley, Sandra E
APPLICANT: Wiler, Scott W
APPLICANT: Szabo, Tomas R.
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
S-09-810-644-32
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                                                                                                                                                                                                                                                                                                           Query Match 94.2%; Score 1454; DB 9; Length 298; Best Local Similarity 92.6%; Pred. No. 3.5e-147; Matches 274; Conservative 13; Mismatches 9; Indels
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
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Clevenger, William
Wiley, Sandra Bileen
Wiler, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                   QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                          VQGIIIYRAAYEGIYDTAKGMLFDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: DRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANTITITE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                       APPLICANT: Anderson,
APPLICANT: Davis, Rol
APPLICANT: Clevenger
APPLICANT: Wiley, Sa
APPLICANT: Willer, Sc
APPLICANT: Scabo, Too
APPLICANT: Ghosh, Soo
APPLICANT: Moos, Wall
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CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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Best Local Similarity
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APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
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nilarity 92.6%; Pred. No. 3.5e-147;
Conservative 13; Mismatches 9;
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; ORGANISM: Homo sapien
US-09-810-644-31
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US-09-810-644-31
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
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Patent No. US20020012992A1
                                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT:
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GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                              MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                              MGDHAWSFLKDFLAGAVAAAVSKTAVAFIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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Moos, Walter H.
Pei, Yazhong
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                                                                                                                                                                           Conservative
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87.2%; Pred. No. 7.5e-140;
ative 21; Mismatches 16;
                                                                                                                                                                        89.8%; Score 1385.5; DB 9
87.2%; Pred. No. 7.5e-140;
ative 21; Mismatches 16;
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RESULT 10
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; ORGANISM: Homo
US-09-185-904A-31
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SEQ ID NO 31
LENGTH: 297
                                                                                                         Sequence 32501, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.8%;
Best Local Similarity 87.2%;
Matches 260; Conservative 2
     APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HARZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PRODUCTION TITLE OF INVENTION: TRANSLOCUTION THEREFOR
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FILE REFERENCE: AEOMICA-X-2
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Willer, Scott W.
Szabo, Tomas R.
Szabo, Tomas R.
Ghosh, Sounitra S.
Ghosh, Sounitra S.
PRODUCTION OF ADENINE NUCLEOTIDE
OVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
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Pred. No. 7.5e-
21; Mismatches
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.5e-140;
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US-10-032-585-7194
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US-10-032-585-7194
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32501
LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7194
LENGTH: 301
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Best Local (
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OTHER INFORMATION: EXPRESSED II
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OTHER INFORMATION: EXPRESSED II
OTHER INFORMATION: EXPRESSED II
OTHER INFORMATION: EXPRESSED II
OTHER INFORMATION: SWISSPROT H.
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APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Local Similarity 93.3%;
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  184
                                         123
                                                                                                                                                                                                                                                                                                        tch 51.1%; Score 788.5; DB 12; Length 301; al Similarity 54.7%; Pred. No. 6.3e-76; 162; Conservative 42; Mismatches 83; Indels 9;
                                                                                  126 TSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
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                                                                                                                                                                                                                 NPFVDPMMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKQGRLEKRYTGIVDCFKRTAADE 64
                                                                                                                                                                                                                                          SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRIPKBQ 65
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                                         TSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGFGPSVIG 182
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EXPRESSED IN LUNG, SIGNAL = 1.

EXPRESSED IN HELA, SIGNAL = 3.5

EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

EXPRESSED IN BRAIN, SIGNAL = 0.95

EXPRESSED IN BONE MARROW, SIGNAL = 0.96

SWISSPROT HIT: P05141, EVALUE 2.00e-83
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Pred. No. 1.2e-78;
6; Mismatches 5;
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US-09-734-569-170
(S-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/60,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PILING DATE: 1999-10-20
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 49.3%; Score 760.5; DB 10; Length 318;
Local Similarity 53.7%; Pred. No. 6.8e-73;
tes 159; Conservative 42; Mismatches 86; Indels 9;
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                                                                                                                                                                                           GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                                                                                                                                                                                                                              TSLCFVYPLDFARTRLAAD--VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
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Milne, Todd
No. US20020128250Alman,
Royer, John
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Silva, Jeff
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Madden, Kevin
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t, Peter
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RESULT 14
US-10-128-714-3338
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SEQ ID NO 170
IENGTH: 386
TYPE: PRT
ORGANISM: Physcomitrella patens
                                                        APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
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NUMBER OF SEQ ID NOS: 181
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                 APPLICATION NUMBER: US 60/287,066
FILING DATE: 2001-04-27
APPLICATION NUMBER: US 60/295,890
FILING DATE: 2001-06-05
APPLICATION NUMBER: US 60/303,899
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Bischoff, Friedrich
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Petra
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53.4%; Pred. No. 1.
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PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: US 60/
PRIOR PILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 3338
LENCTH: 308
TYPE: PRT
                                                                                        ; ORGANISM: Aspergillus fumigatus US-10-128-714-8338
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/297,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
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US-10-128-714-8338
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                                                                                                                                                                                      SEQ ID NO 8338
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                 Query Match
Best Local Similarity
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APPLICANT: Hu, Wenqi
APPLICANT: Tiahkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Excephkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
                                                                                                                                       LENGTH: 30
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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47.8%; Score 737; DB 15;
51.7%; Pred. No. 2.1e-70;
ative 47; Mismatches 85;
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complete : 25	241 244	182 184	124 124	65 A	7
Search completed: December 18, 2003, 12:55:44 Job time : 25.3606 secs	241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298	182 QGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240 : : : : : : : : : : : : : : : : : : : : : : : : :	124 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181 	64 EQGYLSFWRGNLANVIRYEPTQALNEAFKDKYKQIELGGVDKHTQFWRYEAGNLASGGAA 123	7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK 63 : :: : : : : : : 7 AFTDSFAVGGVSAAVSKTAAAPIERIKLLVQNQDEMIRAGRLDRKYNGIIDCFRRTAQ 64

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Result
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Copyright (c) 1993 - 2003 Compugen Ltd.
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29		41 370.5 24.0 415 2 748171 hypothetical prote 42 369.5 23.9 381 2 T51158 hypothetical prote 43 368 23.8 475 2 T50686 peroxisomal Ca-dep 44 363 23.5 348 2 D84798 probable microchond 45 344.5 22.3 332 2 T47703 Ca-dependent solut **RESULT 1** S03894 ADP, ATP Carrier protein T3 - human N; Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP, ATF C; Species: Homo sapiens (man)	hypothetical prote hypothetical prote peroxisomal Ca-dep probable mitochond Ca-dependent solut
	· · · · · · · · · · · · · · · · · · ·	N;Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochon C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C;Datesion: 803894; B28116 C;Accession: 803894; B28116 R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. J. Mol. Biol. 206, 261-280, 1989 A;Title: DNA sequences of two expressed nuclear genes for human mitochondri A;Reference number: 803893; MUID:89236396; pMII:2541251	<pre>lentification); mitochondrial ADP,ATF itext_change 17-Mar-2000 itext_thange 17-Mar-2000 itext_than than the condrial ADP/ATP tr itext_than than the condrial ADP/ATP tr itext_than the condrian than the condria</pre>
a a a rinted,	· · · · · · · · · · · · · · · · · ·	A;Reference number: \$03893; MUID:89236396; PMID:2541 A;Accession: \$03894 A;Status: not compared with conceptual translation A;Molecule type: DNA A;Mesidues: 1-298 <coz> R;Houldsworth, J.; Attardi, G.</coz>	.251
lon state		Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the A;Reference number: A94197; MUID:88124845; PMID:2829183 A;Accession: B28116 A;Molecule type: mRNA A;Residues: 36-104, 'R',106,'A',109-298 <hou> A;Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723</hou>	are expressed at the mRNA level in 183 36750.1; PID:g339723
parrier pr parrier pr pucleotide parrier pr		C;Genetics: CIVEL C;Genetics: ANT3Y A;Gene: GDB:ANT3; ANT3Y A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000 A;Cross-references: GDB:22.32-Xp22.32; Yp11.3-Yp11.3	3000
arrier pr arrier pr arrier pr arrier pr lcal prote lcal prote lcal prote	•	A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB: C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <mat> F;5-99/Domain: ADP,ATP carrier protein repeat homology <acp1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <acp2> F;110-209/Domain: ADP,ATP carrier protein repeat homology <acp3></acp3></acp2></acp1></mat>	tt of sequences for GDB:ANT2 an ler protein repeat homology rransmembrane protein dicted <mat> 99 <acp1> bology <acp2> bology <acp3></acp3></acp2></acp1></mat>
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arrier pr arrier pr arrier pr arrier pr land prote		Db 1 MTBQAISFAKOPLAGIAAAISKTAVAPIERVKLLIQVQHASKQIAADKQXKGIVDCIVR OY 61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG	'QHASKQIAADKQYKGIVDCIVR 60 FLGGVDKHTQFWRYFAGNLASG 120
parrier pr parrier pr parrier pr		Qy 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS	DCLVKITKSDGIRGLYQGFSVS 180

GDB

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J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP
A;Reference number: A29132; MUID:87166056; PMID:3031073
A;Molecular the third state of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
                                                                                           A;Molecule type: mRNA
A;Residues: 1-298 <BAT>
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
                                                                                                                                                                                                                                                                                                          N;Alternate names: mitochondrial ADP,ATP translocase 2
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #text_change
C;Date: 17-Mar-2000 #text_change
C;Accession: A29132; C28116
R;Battini, R; Ferrari, S; Kaczmarek, L; Calabretta, B; Chen,
J, Biol. Chem. 262, 4355-4359, 1987
J, Biol. Chem. 262, 4355-4359, 1987
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A;Title: Two bovine genes for mitochondrial ADP/ATP translocase A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
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C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar 1993 #sequence_revision 03
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A; Title:
                                    R;Houldsworth, J.; Attardi, G
Proc. Natl. Acad. Sci. U.S.A.
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R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker,
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Best Local
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   Two distinct genes for ADP/ATP
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97.7%;
G.
A. 85, 377-381, 1988
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          are
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          mRNA level
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR

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A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology c;Keywords: duplication; homodimer; homocomption; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACPl> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                      A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein : C;Keywords: duplication; transmembrane protein : C;Keywords: duplication; transmembrane protein : R;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: I60173

R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, Biochim. Biophys. Acta 1152, 192-196, 1993

A;Title: Isolation and characterization of CDNA cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: clone pHAT3 C; Genetics:
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A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1;
                                                                                                                                                                                                                              A;Gene: anc.
                                                                                                                                                                                                                                                                           A;Residues: 1-298 <RES>
A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: I60173; MUID:94002161; A; Accession: I60173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenine nucleotide translocator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
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A;Accession: C28116
                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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  Conservative
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                92.3%;
89.6%;
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  18;
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Score 1424; DB 2;
Pred. No. 2e-118;
8; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1454; DB 1;
Pred. No. 4.5e-121;
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  13;
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                                               Length 298
    Indels
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ADP,ATP carrier protein T1 - bovine
N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius teurus (cattle)
C;Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP A;Note: located in the inner mitochondrial membrane C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; m F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Jomain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                        Bur. J. Biochem. 227, 730-733, 1995
A;Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial A;Reference number: S69369; MUID:95172058; PMID:7867632
A;Accession: S69369
A;Molecule type: protein
A;Residues: 49-63;154-168 <OET>
C;Comment: This protein is synthesized in the cytosol and transported into the mitoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 205-298 <BAB>
R;Oettmeier, W; Masson, K; Kalinna,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: residue 52 may be methyllysine R; Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M. Biochim. Biophys. Acta 670, 176-180, 1981
A; Title: Amino acid sequence determination of the ADP, ATP A; Reference number: A61343; MUID:82046808; PMID:6271240
A; Accession: A61343
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A;Residues: 208-298 <ARS>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
R;Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.
R;Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A;Title: Complete amino acid sequence of the ADP/ATP carrier
A;Reference number: A03181; MUID:82188267; PMID:7076130
A;Accession: A03181
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C; Function:
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A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
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A;Accession: A24822
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A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M24102; NID:g529414; R;Rasmussen, U.B.; Wohlrab, H.
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A;Gene: ANC1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein 1
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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N;Alternate names: adenine nucleotide c
;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S37210
R;Laplace, C.; Costet, P.
submitted to the EMBL Data Library, Seg
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C;Genetics:
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A; Residues: 1-298 < LAP >
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Best Local
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKKVI
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                                                                                            VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGKGSSQRBFNGLGDCLTKIFKSDGLKGLYQGFSVS
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Pred. No. 3.le:
19; Mismatches
                                                                                                                                                                                                                                                                                                                                             Score 1418; DB 2;
Pred. No. 6.9e-118;
.9; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 298;
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QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298

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ADP,ATP carrier protein T1 - human
ADP,ATP carrier protein T1 - human
N,Alternate names: mitochondrial ADP,ATP translocase 1
C;Species: Homo sapiens (man)
C;Spate: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A44778; S03893; A39891; A28116
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.
J. Biol. Chem. 264, 13998-14004, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 4035-4035
A; Map position: 4045-4035
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein g; 2-299/Froduct: ADP, ATP carrier protein #status predicted <AMT>
F; 2-299/Froduct: ADP, ATP carrier protein repeat homology <ACP1>
F; 5-99/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP3>
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R;Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: cDNA sequence of a human skeletal muscle ADP/ATP ta A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891
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J. Mol. Biol. 206, 261-280, 1980; Walker and the sequences of two expressed nuclear genes for human mitochom A;Title: DNA sequences of two expressed nuclear genes for human mitochom A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03893
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A;Title: A human muscle adenine nucleotide translocator gene has four exons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-37 < HOU>
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: I-15,'A','I-146,'RR',149,151-226,'L',228-298 <NEC>
A;Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
A;Experimental source: clone pHMANT
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A;Accession: A44778
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                                                       GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                    MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                              I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                           I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                  91.3%; Score 1409; DB 1;
88.3%; Pred. No. 4.3e-117;
   PLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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ADP,ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936
R;Beard, C.B.; Crews-Oyen, A.B.; Collins, F.H.
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S31814
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
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A;Cross-references: EMBL:X70847
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                A; Molecule type: DNA
A; Residues: 1-301 <BEA>
                                                                                                                          A;Status: preliminary
                                                                                                                                         A; Reference number: S31935
A; Accession: S31935
                                                                                                                                                                                 R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier
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A; Accession: S31814
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89.2%;
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Pred. No. 9.8e-
16; Mismatches
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A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP
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A;Accession: T23207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein K01H12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A;Experimental source: clone K01H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-313 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; McMurray, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 207; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: CESP:K01H12.2
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Best Local
                                                                                                   188
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263
                           247 ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKKVI 298
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                                                                                    RAAYEGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGRKG
                                                                                                                                                         LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                                                                                                                                                              LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTEQA--ISFAKDFLAGGIAAAISKTAVAPIERVKLLIQVQHASKQIAADKQYKGIVDCI 58
                                                                                                                                  LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                      AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                                                                                                                                                                                                                                                           FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
                                                                                                                                                                                                                                                                                           PAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMQSWPCKSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVKALL:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTKKADPYGFAKDFLAGGISAAVSKTAVAPIBRVKLLLQVQAASKQIAVDKQYKGIVDCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGAAGATSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFN
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                carrier protein; ADP,ATP carrier protein repeat
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77.0%;
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70.9%;
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                                                                                                                                                                                                                                                                                                                                              Score 1041; DB 2;
Pred. No. 1.7e-84;
29; Mismatches 52;
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Pred. No. 3.6e-97;
3; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                              Length 313;
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A; Map position: 3
A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
                                                                                                                                                                                                                                                   A;Reference number: Z20024
A;Accession: T25371
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-313 <GEI>
A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022;
A;Experimental source: strain Bristol N2; clone T01B11
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T25850
                                                                                                                                                                        A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; A;Experimental source: clone T27E9
                                                                                                                                                                                                                                                                                                                                                                          C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T25850
R;Geisel, C., Stelly
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                                                                                                                                     A;Gene: CESP:T27E9.1
                                                                                                                                                                                                                    A; Residues: 1-300 <WIL>
                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                       R;Lloyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                          T25371
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                                                                                                                                                                                                                                                                                                                                                      Accession: T25371
                                       Query Match
                                                                                                                                                        Genetics:
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  Matches 202;
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                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 AALWRGNLANVIRYFETQALNEAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAAYFGYYDTAKGML-PDPKNTHIVVSWMIAQTYTAVAGVVSYPFDTYRRMMMQSGRKG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAAYFGMFDTAKMVFTADGKKLNFFAAWAIAQVVTVGSGILSYPWDTVRRRMMQSGRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
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  Conservative
                                                                 115/2 carrier protein; ADP,ATP carrier protein
                  67.3%; Score 1038; DB 2; 69.2%; Pred. No. 3e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 1039; 70.9%; Pred. No. 2.
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                                                                                                                                                                                                                                                         from
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    Mismatches
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  49;
                                       Length 300;
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  Indels
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                                                                                                                                                                                               CESP:T27E9.1
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A;Map position: 1
C;Superfamily: ADP,A7
F;9-103/Domain: ADP,F
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C;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-300 <LET>
A;Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z18308
A; Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Le,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein W02D3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
;Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                            VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRR
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                                                                    MMMQSGRK--DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHL
                                                                                           MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKV
                                                                                                                                        VSVQGIIIYRAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRR
                                                                                                                                                                                                          SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF
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                                                                                                                                                                                                                                                                                                 VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA
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ce: strain Bristol N2; clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                              64.4%; Score 993.5; DB 2 64.8%; Pred. No. 2.6e-80;
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RESULT 14

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SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAAD--KQYKGIVDCIVRIPKE

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A;Residues: 1-339 <hIL>
A;Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
A;Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
A;Csuperfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <acptive protein repeat homology <a href="#">ACP3</a>)</a>
                                                                                                        A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat home
C;Keywords: duplication; transmembrane protein
F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP,ATP carrier protein - malaria parasite (Plasmod N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum C;Date: .07-May-1995 #sequence_revision 01-Sep-1995 C;Accession: S68993; S51132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde A;Fifterence number: A41677, MUID:92084708; PMID:1748677
A;Accession: A41677
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C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: A41677
                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-301 < HAT>
                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: S68993
                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Molecular characterisation of the A; Reference number: S68993; MUID: 95188918;
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                             Local
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Biochem. 228, 86-91, 1995
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183;
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                             Similarity
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Score 943; DB 2;
Pred. No. 7.6e-76;
5; Mismatches 62;
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Pred. No. 7.1e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                            ADP/ATP-transporter
PMID:7883016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Plasmodium falciparum)
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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                    Q8SQM5
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OBagh5 bos taurus
OBjhi0 brachydanio
O46373 oryctolagus
O919m9 xenopus lae
O8bvi9 mus musculu
O9prh1 rana rugosa
O99r2 rana rugosa
O99r24 rana rugosa
O99r44 ethmostigmu
O91336 rana sylvat
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45	44	43	42	41	40	39	38	37	36	35	3 4	ω S	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
749	753	756.5	759	760	764	767.5	778.5	827	924	924	932	936	943	944	944	946.5	947	973.5	993	993.5	996	1036.5	1038	1039	1041	1119	1137.5	1159
48.5	48.8	49.0	49.2	49.3	49.5	49.7	50.5	53.6	59.9	59.9	60.4	60.7	61.1	61.2	61.2	61.3	61.4	63.1	64.4	64.4	64.5	67.2	67.3	67.3	67.5	72.5	73.7	75.1
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Q8j0u1 gaeumannomy	Q26697 trypanosoma		074260 candida par	076286 trypanosoma	_	Q8j0m2 yarrowia li	Q9p8ml yarrowia li	Q9xs69 sus scrofa	Q8mvr6 nyctotherus	Q8mvr5 nyctotherus	Q8mvr8 nyctotherus	Q8mvr7 nyctotherus	Q26006 plasmodium	Q8mvr4 euplotes sp	Q25692 plasmodium	Q9xm22 ascaris suu	Q8ij34 plasmodium	Q9bj36 toxoplasma	Q17407 caenorhabdi		O97470 dictyosteli	Q8h727 phytophthor	O45865 caenorhabdi	P91410 caenorhabdi			O62526 drosophila	Q8bkq5 mus musculu

ALIGNMENTS

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Qy 121 GA 	. Qy 61 IP	Qy 1 MT	Query Match Best Local Similarity Matches 277; Conser		RT and ANT mRNA in chicke RL FEBS Lett. 0:0-0(2002)			OC Archosauria		OS Gallus gallus				AC Q8AYM3;	Q8AYM3	RESULT 1
GAAGATSLCFVYPLDFARTKLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 	IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 	MTEQAISPAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR : :	95.5%; Score 1474; DB 13; Length 298; Wilarity 93.0%; Pred. No. 2.5e-125; Conservative 14; Mismatches 7; Indels 0; Gaps	EMBL; AB088686; BAC15533.1; SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;	and ANT mRNA in chicken skeletal muscle."; FEBS Lett. 0:0-0(2002).	"Cold-induced mitochondrial uncoupling and expression of chicken UCP	9031;	ArchoBauria; AVes; Neognathae; Galliformes; Fhasianidae; Fhasianihae; Gallus.	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,	.us (Chicken).	iporter.	(TrEMBLrel. 23,	(Trambirel 23, Created)	-	PRELIMINARY; PRT; 298 AA.	
180 180	120 120	60														

Q8ira0 drosophila Q9nhw5 lucilia cup O44093 drosophila O44094 drosophila Q25129 halocynthia

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01-OCT-2002
01-OCT-2002
01-MAR-2003
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Q8SQH5;
01-JUN-2002
01-JUN-2002
01-MAR-2003
Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio.
                                                                                                               01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Solute carrier family 25 mem
                                                                                                                                                                                                                                           Q8JHI0
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Yamazaki N., Shinohara Y., Tanida K., Terada H.;

Yamazaki N., Shinohara Y., Tanida K., Terada H.;

"Structural properties of mammalian mitochondrial ADP/ATP carriers:

identification of possible amino acids that determine functional
differences in its isoforms.";

Mitochondrion 1:371-379 (2002).

Mitochondrion 1:371-379 (2002).
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Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                SLC25A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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                                                                                                                  22, Last sequence update)
23, Last annotation update)
member 5 protein.
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Pred. No. 3e
                        ; Craniata;
Teleostei;
                                                                     (Danio rerio).
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                      Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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Best Local Similarity
Matches 274; Conser
                 J. Biochem. 335:541-547(1998).

-!- SIMILARITY: BELONGS TO THE MITOCHO
EMBL, AB09386; BAA2377.1;

InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr;-3.

PRINTS; PR00926; MITOCARRIER.

PRINTS; PR00926; MITOCARRIER.
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
SEQUENCE 298 AA; 32763 MM; D78663C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O46373 PRELIMINARY;
O46373;
O1-JUN-1998 (TrEMBLrel. C
O1-JUN-1998 (TrEMBLrel. C
O1-MAR-2003 (TrEMBLrel. 2
ADP/ATP translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolae
                                                                                                                                                                                                                       regulates calcium release from skeletal muscle.";
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Skeletal mu
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Insertional mutagenesis in zebrafish rapidly identifies essential for early vertebrate development.";
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Burgess S., Haldi M., Artzt K., Farrington
Hopkins N.;
                                                                                                                                                                                                                                                                          Yamaguchi N., Kasai M.;
"Identification of a 30kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 31:135-140(2002).
EMBL; AF506216; AAM34660.1; -
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MEDLINE=22035902; PubMed=12006978;
Golling G., Amsterdam A., Sun Z.,
     PRINTS; PR00784; MTUNCOUPLING
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Last sequence update)
Last annotation update)
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Pred. No. 8.5e-123;
L5; Mismatches 9;
                                                                                                                                                                              MITOCHONDRIAL
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Lin S.-Y.,
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                                                                                                                                                                                                                                                                                                  A Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;

T "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific a Dynamic Patterns of Expression During Development.";

Dynamic Patterns of Expression During Development.";

L Submitted (FEB-2000) to the RMBI/GenBank/DDBJ databases.

C -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL; AP231347; AAF63471.1; -.

R InterPro; IPR001993; Mitoch_Carrier.

InterPro; IPR001993; Mitoch_Carrier.

InterPro; IPR002067; Mit_carrier.

InterPro; IPR002030; Mit_uncoupling.

PFAm; PF00153; mito carri 3.

R PFINTS; PR00926; MITOCH_CARRIER.

PRINTS; PR00926; MITOCH_CARRIER; 3.

Membrane; Transmembrane; Transport.

O SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
                                                                                                                                                                                                                                    Query
Best I
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Eukaryota; Metazoa; Anura; Mesobatrachia; Pipoidea; Pipidae;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Venopodinae; Xenopus.
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Q919M9;
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01-OCT-2000
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Local
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(TrEMBLrel. 23, Last annotation update)
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Pred. No. 1.3e-120;
0; Mismatches 13;
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Pred. No. 1.6e-120;
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                                                                                          OSPRH1 PRELIMINARY;
OSPRH1;
O1-MAY-2000 (TIEMBLIEL 13,
O1-MAY-2000 (TIEMBLIEL 13,
O1-MAR-2003 (TIEMBLIEL 23,
ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Bukaryota, Metazoa, Chordata,
Amphibia, Batrachia, Anura, Ne
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Nature 420:563-573(2002).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Solute carrier family 25.
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"The origin and differentiation of the heteromorphic sex chromosomes are z, W. X, and Y in the frog Rana rugosa, inferred from the sequences of a sex-linked gene, ADP/ATP translocase.";

RI a sex-linked gene, ADP/ATP translocase.";

RI -:- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

C:- -- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

REMBL; AB008463; BAA36513.1; --

REMBL; AB008465; BAA36511.1; --

REMBL; AB008466; BAA36511.1; --

REMBL; AB008466; BAA36512.1; --

REMBL; AB008467; MATSCALL; --

REMBL; AB008467; MATSCALL; --

REMBL; AB008467; MIt_carrier.

InterPro; IPR002030; Mit_carrier.

InterPro; IPR002030; Mit_carrier.

InterPro; IPR002030; Mit_carrier.

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DR PRINTS; PR00926; MITOCARRIER.

RROSITES; PS00215; MITOCARRIER.

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01-MAY-2000
"The origin and differentiation of the heteromorphic & Z, W, X, and Y in the frog Rana rugosa, inferred from a sex-linked gene, ADP/ATP translocase.";
Mol. Biol. Evol. 15:1612-1619(1998).

-- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER | EMBL; AB008460; BAA36510.1; -- EMBL; AB008459; BAA36509.1; --
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ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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Matches
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                                                                  InterPro; 15000153; mito_carr; 3.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00715; MITOCH_CARRIER; 3.
PROSITE; PS00715; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
Membrane; Transmembrane; 15B270ED37099A00 CRC64;
                                                                                                                                                                                                                                                                         InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR007984; MTUNCOUPLING.
PROSITS; PR007984; MITOCL CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33082 MW; B0E225E867599A06
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Q9YIC4;
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01-MAY-1999 (TREMBLIEGL 10,
01-MAR-2003 (TREMBLIEGL 23,
                                                                                                                                                                                                              InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana rugosa (Wrinkled frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP/ATP translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99083429; PubMed=9866197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8410;
Local Sim
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88.3%; Pred. No. 3.6e
tive 20; Mismatches
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    Score 1402; DB 13;
Pred. No. 8.3e-119;
1; Mismatches 15;
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annotation update)
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Ranidae; Rana
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RESULT 11
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Best Local S
Matches 243
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Q95VX4;
01-DEC-2001 (TEMBLEEL 1
01-DEC-2001 (TEMBLEEL 1
01-DEC-2001 (TEMBLEEL 1
01-MAR-2003 (TEMBLEEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rubripes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401758; AAL02100.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCHARAIER.
PROSITE; PR00215; MITOCH_CARRIER; 3.
SEQUENCE .299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;
       Q91336
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Pleurostigmophora; Scolopendromorpha; Scolopendridae;
NCBI_TaxID=62613;
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Ethmostigmus rubripes.
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       PRELIMINARY;
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81.5%; Pred. No. 1.56
tive 26; Mismatches
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CG16944-PC.
                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexaspoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Cai Q., Storey K.B.;

L. Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

L. Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

C. -- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.

C. EMBL; U44832; AAA97882.2; --

R. InterPro; IPR001993; Mitoch carrier.

R. InterPro; IPR002067; Mit_carrier.

R. PFANT'S; PR00153; mito carr; 3.

R. PRINT'S; PR00926; MITOCHARRIER.

R. PROSITE; PS00215; MITOCH_CARRIER; 3.

R. PROSITE; PS00215; MITOCH_CARRIER; 3.

Membrane; Transmembrane; Transport.

W. Membrane; Transport.

SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
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Best Local Similarity
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Cai Q., Greenway S.C., Storey K.B.;
"Differential regulation of the mitochondrial
in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana sylvatica (Wood frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
NCBI_TaxID=45438;
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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barlaw R.M., Boyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Mank H.J., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Mank J.F., Agbayani A., An H.J., Andrews-Ffannkooth C., Baldwin D.,
RA Ballew R.M., Basun A., Buck J., Barokstein P., Brottier P.,
RA Ballew R.M., Basun D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Barlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek R., Gong R., Gorrell J.H., Gu Z., Guan P., Harris M.C.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mender D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Halazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
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Ra Shue B.C., Siden R., Roches G., Thong W
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                                                                                                                                             Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smuthiak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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Adams M.D., Celniker
Submitted (MAR-2000)
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Best Local Similarity
Matches 237; Conser
                                                                                                                                                                                                                                                                                                                                                                           Chen Z., Fair J.A., Batterham P.;

"A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AF218587; AAF32322.1; -.

InterPro; IPR00193; Mitoch carrier.

InterPro; IPR002067; Mit carrier.

InterPro; IPR002167; Mit carrier.

Pfam; PF00153; mito carr; 3.

PRINTS; PR00215; MITOCARRIER; 3.

Membrane; Transmembrane; Transport.

Membrane; Transmembrane; Transport.

SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
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Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
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01-OCT-2000 (TrEMBLrel.
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23; Mismatches
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SEQUENCE
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044093;
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EMBL; AF025798; AAB87883.1; --

EYBLE; AF025798; AAB87883.1; --

EYBLE; FROM 192322; Dpse\sesb.

InterPro; IFR00193; MITOCh_carrier.

InterPro; IFR002067; Mit_carrier.

Pfam; PF00153; mito_carr; 3.

PRINTS; PR00926; MITOCH_CARRIER.

PROSITE; PR00926; MITOCH_CARRIER; 3.

Membrane; Repeat; Transmembrane; Transport.

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Genetica 0:0-0(1997)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                 AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE
                                                                                                                                                                                                                      KATEIIYKNTLHCWATIAKQE-GSAFFKGAFSNVLRGTGGAFVLV 288
                                                                                                                                                                                                                                                                    KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLV 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
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     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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(TIENBLEL 23, Last annotation update)
nslocase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comeron J.M., Chen B., Kreitman
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Pred. No. 2.2e-99;
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
NON_TER 288 288
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeng L.-W., Comeron J.M., Chen B., Kreitman N
Genetica 0:0-0(1997).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF025799; AAB87884.1; -.
FlyBase; FBgn0023237; Dsub\sesB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila subobscura (Fruit fly).
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245
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                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                              QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
KATEIIYKNTIHCWGTIAKQE-GTAFFKGAFSNVLRGTGGAFVLV
                     KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLV
                                                    IIYRAAYFGFYDTAR-MLPDPKNTPIYISWAIAQCVTTVAGIVSYPPDTVRRRMMQSGR
                                                                          IIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGR
                                                                                                           ATSLCFVYPLDFARTRLAADTGKGG-QREFTGLGNCLTKIFKSDGLVGLYRGFGVSVQGI
                                                                                                                                    ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI
                                                                                                                                                                 QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
                                                                                                                                                                                                                    AMGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKB
                                                                                                                                                                                                                                                                                                                               288 AA;
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.M.
                                                                                                                                                                                                                                                                                                                                 31775 MW; 06A1D1E477E81B26 CRC64;
                                                                                                                                                                                                                                                                                       76.7%;
80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen B., Kreitman M.;
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